

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2003, 22:29:11 ; Search time 4708.93 Seconds
(without alignments)
9657.588 Million cell updates/sec

Title: us-09-817-869-2
Perfect score: 2808
Sequence: 1 cctcggttcacattctctgt.....catgtctttctacaaac 2808

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estim:*

4: em_estim:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: qb_est1:*

10: qb_est2:*

11: qb_hic:*

12: qb_est3:*

13: qb_est4:*

14: qb_est5:*

15: em_estfun:*

16: em_estom:*

17: qb_qss:*

18: em_qss_hum:*

19: em_qss_inv:*

20: em_qss_pln:*

21: em_qss_vrt:*

22: em_qss_fun:*

23: em_qss_mam:*

24: em_qss_mus:*

25: em_qss_other:*

26: em_qss_pro:*

27: em_qss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1283.4	45.7	2876	11	AY109642 Zea mays
2	585.6	20.9	812	10	BE052194 GA_Ea003
3	553.6	19.7	909	12	BG444220 GA_Ea002
4	527.2	18.8	926	12	BG444037 GA_Ea002
5	520.8	18.5	946	12	BG445432 GA_Ea002
6	514.6	18.3	794	12	BG648859 EST510478

7	510.4	18.2	819	10	BE054064
8	499.8	17.8	826	13	BM413092
9	489.8	17.4	692	12	BG440097
10	484.4	17.3	654	9	A1726884
11	481.8	17.2	725	12	BG5645187
12	475.2	16.9	697	14	BG117782
13	472.4	16.8	894	10	BH412955
14	469.6	16.7	719	13	B1311853
15	468.2	16.7	693	13	AM256649
16	467	16.6	671	13	B1272765
17	466.2	16.6	846	13	B1308483
18	461.8	16.4	791	14	BG744452
19	460.8	16.4	653	10	BE191120
20	456	16.2	739	14	HQ255288
21	453.4	16.1	630	10	AW308762
22	452.6	16.1	838	14	BG001700
23	449.6	16.0	699	12	BG593748
24	446.8	15.9	671	14	BQ156084
25	436	15.5	747	14	BG870632
26	429.4	15.3	561	9	A1726455
27	429.4	15.3	890	12	BG445852
28	425.8	15.2	665	14	BQ505334
29	425.4	15.1	744	14	BQ001881
30	425	15.1	728	14	HQ999968
31	423	15.1	666	13	B1118697
32	421.8	15.0	594	12	BG454873
33	421.6	15.0	648	14	BQ152649
34	421.6	15.0	656	14	BQ148267
35	421.6	15.0	751	12	BG631201
36	420.6	15.0	744	14	BH817206
37	420.6	15.0	761	14	BQ942466
38	419.4	14.9	694	14	BQ743425
39	419	14.9	587	13	B1974011
40	417.2	14.9	758	17	BH436917
41	413.8	14.7	800	10	BH131122
42	410.4	14.6	729	14	BQ854034
43	410.2	14.6	700	9	AL505240
44	408.6	14.6	903	12	BG444884
45	405.6	14.4	738	14	BQ845291

ALIGNMENTS

RESULT 1	AY109642	Zea mays	CL1830_1	mRNA	linear	HTC 25-MAY-2002
LOCUS	AY109642	Zea mays	CL1830_1	mRNA	linear	HTC 25-MAY-2002
DEFINITION	AY109642	Zea mays	CL1830_1	mRNA	linear	HTC 25-MAY-2002
ACCESSION	AY109642	Zea mays	CL1830_1	mRNA	linear	HTC 25-MAY-2002
VERSION	AY109642.1	GI:2121442				
KEYWORDS	HTC					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	1 (bases 1 to 2876)					
AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Voelkel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morquardt,M. and Tinney,S.V.					
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 2876)					
AUTHORS	Coe,E.C.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-Apr-2002) Maize Mapping Project, University of Missouri, Columbia, Mo 65211, USA					
FEATURES	Location/Qualifiers					
Source	1..2876					
	/organism "Zea mays"					
	/db_xref "MaizeDB:640425"					
	/db_xref "taxon:4577"					
	/clone "CL1830_1"					

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DB 2084 ATCTATGTCATCAAAATGATGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2143
QY 2189 AACATCAACAGAGATCAATGATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2248
DB 2144 AACATCAACAGAGATCAATGATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2203
QY 2249 CAATCAACATCAATGATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2308
DB 2204 CAATCAACATCAATGATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2263
QY 2309 TCATTATGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2368
DB 2264 TCATTATGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2323
QY 2369 GAGTGTGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2428
DB 2324 GAGTGTGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2383
QY 2429 ACATGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2488
DB 2484 ACATGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2443
QY 2489 GAGTGTGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2548
DB 2444 GAGTGTGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2503
QY 2549 GGTGTCATTAATGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2589
DB 2504 GGTGTCATTAATGTCAGACATGTCGATGTCGATCAATGAGTACATTAATAATGATGTCGCC 2544

RESULT 2
BE052194
LOCUS
DEFINITION
GA_Ea0034A15f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0034A15f, mRNA sequence.
ACCESSION
BE052194
VERSION
BE052194.2
KEYWORDS
EST.
SOURCE
Gossypium arboreum.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A., and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
COMMENT
On Jun 8, 2000 this sequence version replaced gi:8379250.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATAGCAGTCACTATAGG
High quality sequence stop: 728.

FEATURES
source
1..812
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0034A15f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"

/lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 240 a 152 c 192 q 227 t 1 others
ORIGIN
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Best Local Similarity 84.7% Pred. No. 3.6e-151;
Matches 668; Conservative 0; Mismatches 120; Indels 1; Gaps 1;
QY 1464 TGCTATTCAGCTGAGAGAACTAGAGATGTTATCATTCCTCCCATCTCTCTGTTATGTC 1523
DB 8 TGCTATTCAGCTGAGAGAACTAGAGATGTTATCATTCCTCCCATCTCTCTGTTATGTC 67
QY 1524 CTGATGACTTTGAGGACATGGAATGTCAGTTGTTAGATGTAATGATGAGAGATGTA 1583
DB 68 CTGATGACTTTGAGGACATGGAATGTCAGTTGTTAGATGTAATGATGAGAGATGTA 127
QY 1584 TTGCTTTCCCTGAGACACTGGAAGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1644
DB 128 TTGCTTTCCCTGAGACACTGGAAGATGCTGATGCTGATGCTGATGCTGATGCTGATG 167
QY 1644 ACATCAITGACGGAAGTATTGAGAGATGTTATCATTCCTCCCATCTCTCTGTTATG 1703
DB 188 ATATCAITGACGGAAGTATTGAGAGATGTTATCATTCCTCCCATCTCTCTGTTATG 247
QY 1704 TTATTTATATGGAATATGATTTGCTTGAAGTTTCTTGAAGTTTCTTGAAGTTTCT 1763
DB 248 TTATTTATATGGAATATGATTTGCTTGAAGTTTCTTGAAGTTTCTTGAAGTTTCT 407
QY 1764 TTAAGCTGAGATATTAATGACATGATTAATGATTAATGATTAATGATTAATGAT 1823
DB 308 TTAAGCTGAGATATTAATGACATGATTAATGATTAATGATTAATGATTAATGAT 467
QY 1824 TTAGCAAGATTGGGACGAGAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1883
DB 368 TTAGCAAGATTGGGACGAGAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 427
QY 1884 AGGTTATATGACAGAGTGGCATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1943
DB 428 AAGGAATCCAGAGAGTGGCATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 487
QY 1944 AATGATGATTAAGATATTTGTCAGCTGCTTAAAGCTGATTAATGATTAATGAT 2003
DB 488 ACATGATGATTAAGATATTTGTCAGCTGCTTAAAGCTGATTAATGATTAATGAT 547
QY 2004 GGAACTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2063
DB 548 GAACTATTTAACTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
QY 2064 AATGTCAGAGAAAAACAGAGATGATGATGATGATGATGATGATGATGATGATG 2123
DB 608 AATGTCAGAGAAAAACAGAGATGATGATGATGATGATGATGATGATGATGATG 667
QY 2124 TCATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2183
DB 668 TCATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 727
QY 2184 CTGCTCAACATCAACAGAGATCAATGATGATGATGATGATGATGATGATGATG 2243
DB 728 CTGCTCAACATCAACAGAGATCAATGATGATGATGATGATGATGATGATGATG 786
QY 2244 CCTATCAAC 2252
DB 787 CCTATCAAC 795
RESULT 3
BG444220
LOCUS
DEFINITION
GA_Ea0023K16f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0023K16f, mRNA sequence.
ACCESSION
BG444220
VERSION
BG444220.1
GI:13454872

Db 2 GGAAGCTCATTTGACTGGGGGGGGGGGGCGTTAAGCCTGAGGATATTAAAGCTTTTCAT 61
QY 1793 CTATATCCCAAGAACTTTTCACTCAAGATACCTTACCAAGATTCGGCGACGGAGAGGTTC 1852
Db 62 CTGATTCCTCAAGAACTTTTCACTTAAATTTTACCAAGATTCAGCAAGAGAGAGGTTC 121
QY 1853 ACTGTTTACATTTGTTTCAATGTTGGCCAGAGGGTATACCAAGAGAGTGCATCAGTTCAG 1912
Db 122 AGCGTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 11
QY 1913 GCTATATATGATTTGGCAGAGACCAATGCAATGATGATATATATATATATATATATAT 1972
Db 182 GCAATATATGATTTGGCAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 241
QY 1973 CTCAGAGCCCAAGAACTTTTGGAGGATTCCTCGCACTATCTGACATCTCTTCCTCTTGGT 2032
Db 242 CTCAGAGCCCAAGAGTACGATGAGATCCAGAACTATTATACATTTTCTGCTTGGG 301
QY 2033 AAGCGGCAAGTGAAGAGAGTGTGATATGAATGATGACCTGCAGAAACCAAGAGGCTGATACA 2092
Db 302 AAGCGGAGAGGTGAAGAGAGTGTGATATGAATGATGACCTGCAGAAACCAAGAGGCTGATACA 361
QY 2093 GACTATATAGAGCTCAGAGAGCCAG-ACGTTTCACTATTTATGTTTATACAAAGATGAT 2151
Db 462 GATTATGCCAGAGCTCAGAGAGCCGCTGCTTTCATGATCTATGTTTATGCTTAAATGAT 421
QY 2152 GATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2211
Db 422 GATTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
QY 2212 TGGTGTAGAGAGTCCGAAATAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 2271
Db 482 TGGTGTAGAGAGTCCGAAATAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 541
QY 2272 GCAGCCAGAGAGGTCAGATCATGTTTCCGTATGCTATGATGATGATGATGATGATGATGATG 2331
Db 542 GGAACAGCAGAGGAGGAGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
QY 2332 CATGCTCGAGAGTCACTTCCCTTAATCCAGAAAGTGGAGAGTGTGAGAAAGTGAACCA 2391
Db 602 CATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
QY 2392 GATGGCAAAATATTTGGATCTTATTCAGCGAGACACTGGAACATGACTGACTGCTG 2451
Db 662 GATGCTGCAAAATATTTGGATCTTATTCAGCGAGACACTGGAACATGACTGACTGCTG 720
QY 2452 TCATTGCTCGGTATGCTATTCGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2511
Db 721 ACAGTACTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 2512 AAGGAGATTTTTCCTGAC 2530
Db 781 GCGGAGTGTCTTCTGAC 799

RESULT 5
LOCUS BG445432
DEFINITION GA_Fa002811lf Gossypium arboreum 7-19 dpa fiber library Gossypium
arboreum cDNA clone GA_Fa002811li, mRNA sequence.
ACCESSION BG445432
VERSION BG445432.1 GI:13455180
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Rosidae: eurosids II: Malvales: Malvaceae: Gossypium.
1 (bases 1 to 946)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Jeslic, A., and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber

JOURNAL
COMMENT

Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Seq primer: TAAATACGACTTACTATATAC33
High quality sequence stop: 572.
location/Qualifiers
1. 946

FEATURES
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/organism: "Gossypium arboreum"
/strain: "AKA"
/cultivar: "H400"
/db_xref: "taxon:29729"
/clone: "GA_Fa002811li"
/clone_lib: "Gossypium arboreum 7 10 dpa fiber library"
/issue: "type="fibers isolated from bolls harvested 7-10
dpa"
/lab_host: "E. coli"
/note: "vector: pBK CMV; Site_1: EcoRI; Site_2: XhoI"
264 a 191 c 253 g 236 t 2 others

BASE COUNT
ORIGIN

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Rest Local Similarity 76.9% Pred. No. 40-144;
Matches 661; Conservative 0; Mismatches 193; Indels 5; Gaps 2;

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Db 63 CAAACTTTCATTCCTTTTCAGAGACACTGATTTGGACACAGCATATGATATTTTCATCAGC 122
QY 1383 ACTCCAGACTTGAAGAGCAATTTGCTTGGATGTTTGTATTTTGAAGCAGATGCA 1442
Db 123 ACTCCAGACTTGAAGAGCAATTTGCTTGGATGTTTGTATTTTGAAGCAGATGCA 182
QY 1443 GAAAGCAAGTGTAAAGACCTGCTCATTCAGTGTAGAGCAACTAGAGATGTTATCATT 1502
Db 183 AAGCAGAGAGGCTAAAGAGTGTCTTTCAGCTGAGAGCAATTTGAAGATGTTATCATT 242
QY 1503 CCCCATCTCTGTTATGTAATCTGATGATTTTTCAGCATGATGATGATGATGATGATGAT 1562
Db 243 CCCCATCTCTGTTATGTAATCTGATGATTTTTCAGCATGATGATGATGATGATGATGAT 402
QY 1563 CCATTGATGTTGAGTGTGATTTGTTTTCAGCATGATGATGATGATGATGATGATGATGAT 1622
Db 303 CAATTGATGTTGAGTGTGATTTTTCAGCATGATGATGATGATGATGATGATGATGATGAT 362
QY 1623 GGTTCCTGAGTGAAGAGTATACATGATGATGATGATGATGATGATGATGATGATGATGAT 1682
Db 363 GGTTCCTGAGTGAAGAGTATACATGATGATGATGATGATGATGATGATGATGATGATGAT 422
QY 1683 CCATTGAGAGGCAAGAAATTTTATTTATTTGAAAATTCAGTATTTCTTGGAGTTCCT 1742
Db 423 CTATAGCAGAGCAAGAAATTTTATTTATTTGAAAATTCAGTATTTCTTGGAGTTCCT 482
QY 1743 TTGTTGGAGTCTGATGTTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1802
Db 483 TTGACTGAGTCTGATGATTTAAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 942
QY 1803 AGAACTTTTATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
Db 543 AAGAACTTTTATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602
QY 1863 TTCTTCTCAATGTCGACAGAGGATATACACAGAGTGTGATGATGATGATGATGATGAT 1922
Db 603 TTGATGAGGCTGATGTCGACAGAGGATATACACAGAGTGTGATGATGATGATGATGATGAT 662

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Db	663	ATTCGGGAGAAGACGATGACATGATGTGTGAAGATGGTGATGCAAGTCTATGAGCC	722
QY	1982	AATGGAATATTGAGGATGCTCGCAACTATCTGATCTGATCTGCTTAAAGGCG----	2048
Db	723	CGGGTGTGGTGAGTATCCAGACACTTTGCGAGTCTTTTGTGCGCTGTGGACCGCGGN	782
QY	2019	-GAAGTGAAGAAAGTGTGCTGAATATGACACCTGTGAGAAAAACACAGAGCTGATACAGACTA	2047
Db	783	AGTAGAAGACAGTGGAGTATATGAGACCGGGTCAGAAAAAGCTACGCTATGTCNGATTG	842
QY	2098	TATAAGAGCTTCAGAGGCC	2116
Db	843	TACCAAGACTCGAGAGGCC	861
RESULT	6		
LOCUS	BC648859		
DEFINITION	EST510478 HOGA Medicago truncatula cDNA clone phOGA-2467 5' end,	794 bp mRNA linear	EST 24-APR-2001
ACCESSION	BC648859		
VERSION	BC648859.1	GI:14784971	
KEYWORDS	EST,		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.		
REFERENCE	1 (bases 1 to 794)		
AUTHORS	Bahn,M.G., Ojane-Kuuls,T., Samac,D., Town,C.D., Van Aken,S., Uitterback,T., Cho,J. and Fraser,C.M.		
TITLE	ESTs from roots of Medicago truncatula treated with oligonucleotides of bp 6-20		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Michael G. Bahn Complex Carbohydrate Research Center University of Georgia 220 Riverbend Road, Athens, GA 30602-4712, USA Tel: 706-542-4457 Fax: 706-542-4412 Email: bahno@ccrc.uga.edu		
FEATURES	G932465c TIGR sequence name: MIMCQ40TK More information is available at: www.medicago.org		
SOURCE	Seq primer: SKmod (CTA gAA CTA gTA qAT CC). Location/Qualifiers 1..794 /organism="Medicago truncatula" /cultivar="Al7" /db_xref="taxon:8860" /db_xref="phogA-2467" /clone_lib="HOGA" /tissue_type="3 day old seedling roots" /dew_stage="24 hours after treatment in the dark at 26 C with 0.5 mg/ml oligonucleotides (DP 6-20) in the presence of 100 ug/ml gentamicin" /lab_host="Xl0108"		
BASE COUNT	216 a 143 c 199 g 246 t		
ORIGIN			
Query Match	18.4%	Score 514.6;	DB 12; Length 794;
Best Local Similarity	80.6%	Prod. No. 1.9e-141;	
Matches 649; Conservative	0;	Mismatches 149;	Indels 5; Gaps 3;

LOCUS A1726883 653 bp mRNA linear EST 11-JUN-1999
 DEFINITION RNLG16793 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to [U72693] phospholipase D [R. communis communis], mRNA sequence.
 ACCESSION A1726883
 VERSION A1726883.1 GI:5045735
 KEYWORDS EST.
 SOURCE upland cotton.
 ORGANISM Gossypium hirsutum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Malvales; Malvaceae; Gossypium.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
 TITLE ESTs from developing cotton fiber
 JOURNAL Unpublished (1999)
 COMMENT Contact: Ben Burr
 Biology Department
 Brookhaven National Laboratory
 Upton, NY 11973, USA
 Tel: 516-344-4396
 Fax: 516-344-3407
 Email: burr@bnl.bnl.gov
 Seq primer: T3 Primer.
 FEATURES
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 1..653
 /organism="Gossypium hirsutum"
 /cultivar="Acala Maxxa"
 /db_xref="taxon:3635"
 /clone_lib="Six-day Cotton fiber"
 /tissue_type="Immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="Xil-pluc"
 /note="Vector: pBluescript II KS+"
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 Best Local Similarity 84.0%; Pred. No. 4.2e-123;
 Matches 545; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
 QY 1236 TCACCTCTGTGAGGAGATATGATCCCATTCATCCCTTTTCAGGACACTGGATT 1295
 DB 2 TIGATCTTGTGAGGAGATATGATCCCATTCATCCCTTTTCAGGACACTGGACA 61
 QY 1296 CGGCACACCATGATTTTCATGACCCCACTTTGCTGTGCTGCTCAATGAAAGAGTG 1355
 DB 62 CAGCTCAGCATGATATTTCCATCAGCAAACTTCACTGATGCTTCAATCAGCAAGAGTG 121
 QY 1456 GTCCAGAGAACCTTGGCATGATCCACTCCAGACTTGAAGACCAATTCCTTGGCATG 1415
 DB 122 GACCAAGGAACTTGGCAGATATTCACCTCCGACCTGGAGAGGCAATTCCTGGATG 181
 QY 1416 TTGTGTTAATTTGACAGAGATGAGAAAGCAAGTGTGAAGACCTGCTCATTCAGC 1475
 DB 182 TCTGTTCATTTTGACAAAGATGGAAGAGCGCTGAAGAATGCTCTTCAGC 241
 QY 1476 TGAGAGACTAGAGATGTTATTCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1535
 DB 242 TGAGGAACTTGAAGATGTCATATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
 QY 1536 AGCATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1595
 DB 302 AACTTGAATGTACATATTATGATCAATGATGATGATGATGATGATGATGATGATGAT 361
 QY 1596 AGACCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1655
 DB 362 AGACCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
 QY 1656 GAATATTCAGATGCTTATATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1715
 DB 422 GAATATTCAGATGCTTATATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
 QY 1716 AATATCATTTTCTTCTGGAAGTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1775

DB 482 AAAATCAGATTTCGCGAAGCATTTCATGACGAGGCTCCTGATCAGATTAAGCTGAGG 541
 QY 1776 ATATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1835
 DB 542 ATATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
 QY 1836 CGGACGGGAGAGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1884
 DB 602 AANCAGGAGAGAGTTTACGTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 650
 RESULT 11
 RG645187
 LOCUS RG645187.1 GI:13780299
 DEFINITION EST505806 KV3 Medicago truncatula cDNA clone pKV3-9B9 5' end, mRNA sequence.
 ACCESSION RG645187
 VERSION RG645187.1
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 REFERENCE 1 (bases 1 to 725)
 AUTHORS VandenBosch, K., Hudre, G., Bur, J., Beremand, P., Town, C.D., Bowman, C.L., Craven, M.R., Cho, J. and Fraser, C.M.
 TITLE ESTs from roots of Medicago truncatula 72 h after Rhizobium inoculation, 2001
 JOURNAL Unpublished (2001)
 COMMENT Contact: VandenBosch K
 Department of Plant Biology
 University of Minnesota
 220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
 Tel: 612 624 2755
 Fax: 612 625 1738
 Email: kvandenb@chb.umn.edu
 M393594c TIGR sequence name: MTERY051K More information is available at: www.medicago.org
 Seq primer: SKmod (CTA GAA CTA GTC GAT GC).
 FEATURES
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 /tissue_type="Seedling roots"
 /dev_stage="3 days post-inoculation with Sinorhizobium meliloti"
 /lab_host="E. coli strain XL10R"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the UniZap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL10R cells."
 BASE COUNT 201 a 168 c 179 g 177 t
 ORIGIN
 Query Match 17.2%; Score 481.8; DB 12; Length 725;
 Best Local Similarity 80.2%; Pred. No. 2.4e-122;
 Matches 578; Conservative 0; Mismatches 142; Indels 1; Gaps 1;
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 QY 1931 AAGAGGACAAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1990

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QY	2111	GAGGCACAGAGCTTTCATGATTATGTTTCATACAAAGATGATGATGTCGATGATGATAC	2170
Db	242	CAGCCCGAGCTTTCATGATATATGTTTCATACCAAGATGATGATGATGATGATGATGAT	301
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Db	722	T 722	
RESULT	12		
LOCUS	H0117782		
DEFINITION	EST603458 mixed potato tissues Solanum tuberosum cDNA clone SIMU25	697 bp mRNA linear	EST 22 JUL 2002
ACCESSION	H0117782		
VERSION	H0117782.2	GI:21918492	
KEYWORDS	EST		
ORGANISM	potato		
REFERENCE	Solanum tuberosum		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids 1; Solanales; Solanaceae; Solanum.		
TITLE	Generation of a set of potato cDNA clones for microarray analyses		
JOURNAL	Unpublished (2002)		
COMMENT	on Apr 17, 2002 this sequence version replaced gi:20164744. Contact: Robin Buehl The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potatomicro@igf.org		

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REFERENCE
AUTHORS      Grusak,W.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., Cho
              J. and Fraser,C.M.
TITLE        ESTs from developing reproductive tissues of Medicago truncatula
JOURNAL      Unpublished (2001)
COMMENT      Contact: Michael A. Grusak
              USDA/ARS Children's Nutrition Research Center
              Baylor College of Medicine
              1100 Bates Street, Houston, TX 77030-2600, USA
              Tel: 713-798-7044
              Fax: 713-798-7078
              Email: mgrusak@bcm.tmc.edu
              B398708e

TIGR sequence name: MTPBA751K
More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gTg gAT gAT G).
              Location/Qualifiers
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                      /clone="pGESh15N5"
                      /clone_lib="GESdb"
                      /tissue_type="immature seeds"
                      /dev_stage="immature seeds, 11 to 19 days after
                      pollination"
                      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                      XbaI; Immature seeds, collected from pods ranging in age
                      from 11 to 19 days after pollination, were harvested from
                      greenhouse-grown plants. Seeds were removed and

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[illegible]

Search completed: May 5, 2003, 07:20:29
Job time : 4729.93 secs

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RESULT 2

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US-10-078-770-123
: Sequence 123, Application US/10078770
: Publication No.: US20030003471A1
: GENERAL INFORMATION:
: APPLICANT: Famodu, Omolayo O.
: APPLICANT: Forge, Charlie
: APPLICANT: Miao, Guo-Hua
: TITLE OF INVENTION: cDNAs Encoding Polypeptides
: FILE REFERENCE: BB-1365 US NA
: CURRENT APPLICATION NUMBER: US/10/078,770
: CURRENT FILING DATE: 2002-02-19
: PRIOR APPLICATION NUMBER: 09/614,188
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: 60/143,400
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/153,534
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: 60/161,223
: PRIOR FILING DATE: 1999-10-22
: PRIOR APPLICATION NUMBER: 60/159,878
: PRIOR FILING DATE: 1999-10-15
: PRIOR APPLICATION NUMBER: 60/157,401
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/143,419
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/143,409
: PRIOR FILING DATE: 1999-07-12
: NUMBER OF SEQ ID NOS: 196
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 123
: LENGTH: 2736
: TYPE: DNA
: ORGANISM: Glycine max
US-10-078-770-123

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QY	337	TAGAGTTGGGAGSACTASAACTACTGAAAATGAACAATGCAAGCTCAAGCTGAGTGGTATGAGTC	396
Db	293	AGAGTAGGAGGAGSACTAGAAATCATAGAAATGAACATACTAATGCCAGATGGTATGAGTC	352
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QY	2181	GATCTGCCAACATCAACCAAGAGATCAATGGATGGTGTAGAGACTCGGAAATAGCCATGG	2240
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RESULT 5

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US-09-938-842A-487
: Sequence 487, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCDPI300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 487
: LENGTH: 2571
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-487

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Query Match	15.6%	Score 437.4;	DB 9;	Length 2571;
Best Local Similarity	54.1%	Pred. No. 8.4e-124;		
Matches 1208;	Conservative	0;	Mismatches 908;	
			Indels 117;	Gaps 11;

QY 477 AACCCAGAGTGGHACAGTCCTTTCACGCTTTATTGCTCATCAGCGCTTAAATGTAATA 436
 Ub 422 AATCGTGTGGATGACAGCATTCGATGTACCGCTTGCTCATAGTGCTGTGAAGTACAT 381
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QY 1545 GACGATGGAATTCACAGTTGTTTATGATCATGATGAGTGGAGTGCATTTGCTTCCCT 1594
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DB 1618 ATGACATACATGACGCTTATGTTAAGCGATACGATCTGCTCAGCAGCTTCATTTACAT 1677
QY 1715 GAAAAATGATTTCTTGGAAGTTCTTTTGGTTGAGAGTCTGATGGTATTAAGGCTGAG 1774
DB 1678 GAGAAGCAATATTTCTGGATCTTCTATTCATTCACACTGGCATTCAAA-----CAAG 1725
QY 1775 GATATTAAATGATCATGATCTAATACCAAGGAACCTTTTCACTCANGATATATTACAGAT 1834
DB 1726 GACTTGGTGTCTAATATGCTAATGCTAATGCTGATGGAATCGGCTTAAGATTTCTTAATAAGAT 1785
QY 1835 GCGCAGAGGAGAGTTCACGTTTATATGTTTGTTCATGTCGTCAGAGGCTATACCA 1894
DB 1786 AAGAGGAGGAGAGATTTCTGCTGCTTATATGTCATTCGAATGGGCGAGAAAGTGTCCA 1845
QY 1895 GAGAGTGCATCAGTTCAGGCTATATATTAGATTTGGCAGAGAGACAAATGGAATGATGAT 1954
DB 1846 ACAAGTAAGGCTATTCAAAGAAATCTCTACCTGGCAGCA/AAAACGATGCAAAAGAATAT 1905
QY 1955 AAGCATATTTCTGAGGCTCTCAAGGCAATGGAATTTTG-----AGATCTCTGGAAC 2008
DB 1906 CAAGCATCTACAAAGGCTCTTCTGGAAGTTGGTCTTGTATGGGAGCTTCAGGCGCAAGAG 1965
QY 2009 TATCTGACATCTCTCTGCTTCTGCTTAACCGGAGAGTCAAGAGTGGTGAATATGAACCT 2068
DB 1966 TTTTGAATCTCTCTGCTTCTGGAAGCAGAGATTTGGAGACAGAGGTTCTGTATGGA 2025
QY 2069 GCGAAAA-----ACCAGAGCCTGATACAGACTATATAAGA 2104
DB 2026 ACAGTTAATGATATAATTTCTGCTCGAAGCCACCTCAGCCAAATGCTCGCAGGTGCGAA 2085
QY 2105 GCTCAGAGAGCCACAGCTTTTCATGATTTATGTCATACAAAGATGATGATTTGCTATGAT 2164
DB 2086 GCTTTGAAGAGTCTGAAGATTCATGATATATGTTTCATCTG/AAAGGTATGTTAGTGAATGAT 2145
QY 2165 GACTACATTTAATTTGATCTGCGCAATCAACACAGAGATCAATGATGATGCTGATCAGAG 2224
DB 2146 GATTTTCTCTAATTTGTTGCGGAATATCAACACAGAGATCTTTGGAAGGAAGTACAGAG 2205
QY 2225 TCGAAATAGTCATGGAGGCTATCAACACACATCACTTCTCAACAGGCA-----GGCA 2278
DB 2206 ACTGAATCTCTATGGAGGTAFCAGCCACATCATTCATGGGCTCAAGAAAGCTTCTCGT 2265
QY 2279 GCACAGAGTCAGATCATGATGTTTCTGATGCTATTTATGTTAGTACAGACCTTGGATGCTC 2348
DB 2266 CTCTGGTGTGAGATCTTTGATATAGAAATGCTTTATGAGCAGCAATCATAGAGTTTCTA 2325
QY 2339 GACGAGTCTATCTTAACTCAGAAAGTGGAGGCTGTCAGAAAGTGAACACAGATGCGCA 2398
DB 2326 GACACAGAAATTCAGGAACCCAGAGACATGGAAATGCGTGAGACGAGTTTAGGCAATTTGAT 2385
QY 2399 GAAAAATATTGGGATCTCTATTCAAGCGACACACTGCAACATGACATCTGCTATTTTG 2458
DB 2486 GAGCTGAATTTGGGACAGATATCAACAGAGAGGAGACACA---GAGATGTCAGTCACTT 2442
QY 2459 CTCTGGTATGCTATTGAGGTGGCTAGTGAAGAGATGTCACAGAGCTCTGCTGGAAGGAG 2518
DB 2443 CTTAAGTATGACCTCAATTCAGTCAATAAAGAGG/AAAGTCACTTCTCTCTGATGCGAG 2502
QY 2519 TTTTCTGCTCA 2529
DB 2504 ACATTCGACGA 2513
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RESULT 7
US-10-078-770-143
: Sequence 143, Application US/10078770
: Publication No. US20040004471A1
: GENERAL INFORMATION:
: APPLICANT: Pamada, Omolayo O.
: APPLICANT: Miao, Guo Hua
: TITLE OF INVENTION: cDNAs Encoding Polypeptides
: FILE REFERENCE: BB-1465 US NA
: CURRENT APPLICATION NUMBER: US/10/078,770
: PRIORITY FILING DATE: 2002-02-19
: PRIOR APPLICATION NUMBER: 09/614,188
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: 60/144,400
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/154,544
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: 60/161,224
: PRIOR FILING DATE: 1999-10-22
: PRIOR APPLICATION NUMBER: 60/159,878
: PRIOR FILING DATE: 1999-10-15
: PRIOR APPLICATION NUMBER: 60/157,401
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/144,419
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/144,409
: PRIOR FILING DATE: 1999-07-12
: NUMBER OF SEQ ID NOS: 196
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 143
: LENGTH: 2797
: TYPE: DNA
: ORGANISM: Glycine max
US-10-078-770-143
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Query Match 15.5%; Score 414; DB 9; Length 2797;
Best Local Similarity 54.0%; Pred. No. 10-122;
Matches 1195; Conservative 0; Mismatches 920; Indels 99; Gaps 11;
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QY 377 AACCCAGCTGTATGATGATCTTTCAGGTTATTTGGTCAACAGCTTTCAAACTAAATA 496
DB 294 AACCTGTGTGACACACATTTTAACTGTCGCTTGCACATCTTCTTCAAGCTTCA 654
QY 437 TTCACAGTCAAGACATCAAACTGATTCGAGCACTTAACTGCAACACATATGCAACA 496
DB 354 TTGTGTGTCAAGACAGTCAATATCTGGGTCTCAACATTTATGGGGAACTTCA 415
QY 497 GTTGAAGAGTCTCTATGAGCAACACAGATATATAATGCTGGCTTCAATATGCAACAA 556
DB 414 GGGGAACATTTATGTTAGTGGAAACAAACATCTGAGGCTTCTTCCCAATCTTGGCTAAAT 474
QY 557 AACAACTGCTCATAGTGGTTTAAATATCAATGCAAACTGACATTTTCAAGTAACT 610
DB 474 GCGAAACCATTAACAGCTGGAGTGGTGGTGGTCTTATGATATCACTCACTAACAGCTTCAA 544
QY 617 AAGGAGCTAACTGGAGACAGGATATACAA---CTTCAATAATCTCTGATATAT 674
DB 534 AAGGTGCTCTTTATAGCACTGAGTATGGTGGCTGGATTAAGAAAGGCTGCTGG 694
QY 674 ACATATCTCTGACAGCAAGAGTAAAGTTCTCTCAACAGAGCTCATATATCA 744
DB 594 ACCTACTTCTCTTAGAAAAAGCTGCAAAAATTAATATTTATCAATATCTATCTGAAA 654
QY 744 GACAAATTTGTTCTCAAAATCTCTCTCTGAGTAAATATCAATGAGCTCAAGCTGCT 794
DB 644 GAAGCTGCTCTCTCAATTTGAAGGCTGAGTGAATCTCAATTAACATCAAGCTTCT 714
QY 794 TGGGAACAGCTTTTTCACAGCAATTAACAAAGCAAAACATTCATCAATATCTGCTG 894
DB 714 TGGCAGATATATTTCTATGCAATAAAGTGGGCTCTGCTGATTTGTTATATCTGCTGCTG 774
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QY 854 TCTGTTTACTGAAATCTCTTAATAAGGAGCTCGAGAGGCCAAAGCCAGGAGGAT 913
DB 774 TCTGTTTACTGAAATCTCTTAATAAGGAGCTCGAGAGGCCAAAGCCAGGAGGAT 824
QY 914 ATCAGCTTACGAGTCTGTTAAGAGAGGCAAGTGAAGTGTAGGTCCTCTATGCTG 973
DB 825 TACACTTTAGGAGTCTCTCAAGCCAAATCAGAGGAGGTGTAGAGTGTCTGCTCTT 884
QY 974 GTTGGGATGACAGAACCTC-----CGTTGGTTTATTCAGAAAGGATGATCATGCA 1027
DB 885 GTTGGGATGACCCACGCTCAAAAGCAGCTTGGATTAAACCGTTCGACCTCATGAAC 944
QY 1028 ACTCATGATGAGAGACTGAACATTTCTCCAGAAATCACTGATGTCGATGTGTGTGTG 1087
DB 945 ACTCATGATGAGAGACTGACCCAGTTTTCAGAACTCTTCAGTACGAGTGTCTCTTTC 1004
QY 1088 GCTCGAAATCCCTGATGATGCTGGAAGCTTTGTTCAGGATCTCAAAATCTCTACTATGTC 1147
DB 1005 CTACGAGCTTGGTGGAAAGAGCATAGCTGGGTCAAAACGAGGAGCTGGAACAATCTAT 1064
QY 1148 ACTCATCAGAGAAATTTGGTGTGGAGCTGCAATGCTTAATGGAGATTCGGAGAGG 1207
DB 1065 ACCCATCATCAGAGAGACGTCATTTGGA-----TGCTGATGACAGGTGAGATAAA 1115
QY 1208 AAGAGAAATGTCAGTTTGTGGAGTCTCGACCTCTGTGATGGAGATATGATCCCCA 1267
DB 1116 AGAAAAATCAAGCTTTTATCGAGGCTGTGATTTATGCTGGGCGATATGATACCCA 1175
QY 1268 TCCATTCCTTTTCAGGACATGCGATGCGGACACCATGATTTTCATCAGGCCAAC 1327
DB 1176 AACCATTCATCTTTAGGACTTTGACACACACAAAGATGACTATCATATCTCTAAC 1235
QY 1328 TTTGCTGGTCTCAATTAAGAAAGGTGCTCAACAGAACCTTTGGCATGACATCCACTGC 1387
DB 1236 TTTGAGGGGCC-----AGTACTGCTGTCCAAAGCAACCATGCGCATGTTGCATTC 1289
QY 1388 AGACTTTGAGGACCAATGCTTGGATGTTTGTGTTTAAATTTTGGAGAGAGTG----- 1440
DB 1290 CAAGTTGATGGTCCAGCAGCATATGACATCTCACCAATTTTGGAGGCGTTGTTAAG 1349
QY 1441 -----GAGAAAGCAAGGTGTGAAGACCTGCTCAT 1471
DB 1350 GCATTAAATATCATAGATTTCAAAAGATGAAGATTCACATGATGATTCATTACTGAAA 1409
QY 1472 CAGCTGAGAGAACTAGAGATGTTATCATTCGCCCATCTCTGTTATGATCTCTGATGAC 1531
DB 1410 ATTGATAGAACTCCCTGACATTTGTGCAATTTGATGAAGTTCCTTGCAGAAATGAAAATAAC 1469
QY 1532 TTTGAGCATGGAATGCTCAGTTGTTTAGATCCATTGATGGTGGAGCTGCATTTGGTTTC 1591
DB 1470 CAGGAGACTTGGCATGCCAGGCTCTCCGTTCAATTTGATCTCAATTTCTGTGAAGGATTT 1529
QY 1592 CTTGAGACACCTGAAGATGCGGCGAGAGGCTGGGCTGTGAGTGAAGGATGAACATCAT 1651
DB 1530 CAAAGSAGCCACAATCTATAAAGAGACTTGGTTGTGAAGATGATGATGATA 1589
QY 1652 GAGCAGATATTGAGATGCTTATATCCATGCAATTCGAGGAGGCAAGAAATTTTATTTAT 1711
DB 1590 GAGATGAGCATATATTCAGCGTATGTCAGCAATTCGAGGAGCCCAAGAAATTTATCTAT 1649
QY 1712 ATTGAATATGATTTTCTCTGAGATCTTTTGGTGGAGTCTGATGATGATTAAGCT 1771
DB 1650 ATTGAAGACCAATATCTTCTGCTGCTATATTAATTTGGAATCTTTA-----C 1697
QY 1772 GAGATATTAACTGACTGCACTTAATACCAAGGAACTTCTACTCAAGATCTTAGCAAG 1831
DB 1698 AAGACCTTGGTCAACACACTTAATTCCAATGGAATTCGATTAATAATACCAATAAA 1757
QY 1832 AFTGGGCGAGGAGAGTTCATCTGTTTACATGTTGTTTCCAAATGCGGAGGAGGATATA 1891
DB 1758 ATCAAAACACATCAGAGATTTTCTGTGTATATGTCATTCCTATGTCGCTGAAGGTGTA 1817
QY 1892 CCAGAGTGCATCAGTTTCAAGCTATTATGATTGGCAAGAGGACATGGAATGATG 1951

DB 1818 GCTACAGTACAGCTTACTCAGAGGATTTCTTTTTGGCAGTTTCAAAACAAATCAAAATGATG 1877
QY 1952 TATTAAGAATATGTGACAGGCTCTCAAAAGCCCAATGG-----AAATATCAGCAATTTAGG 2005
DB 1878 TATTAAGAATATGTGACAGGCTCTCAAAAGGCTTGAATAAGATATGAACATAG 1937
QY 2006 AACTATCTGACATTTCTCTGTTTAAAGGCAATTTGAAGAGAGTGTGTAATATGAA 2065
DB 1938 GACTACTTGAATTTCTTTGCTTGGCAATCTGAGATCTGATCTGAAATGAAATGTTTA 1947
QY 2066 CTTGAGAAATAACAGACCTCTGATACACA---CTATATAAGATCTCAGAGAGGAGAGCT 2122
DB 1998 AATCATGTAAAACTACTGAGCAAAACAAAGGCTCAGGCTCACTTAAAGAGAGGAGAG 2057
QY 2123 TTCATGATTTATGTCATACAGAGATGATGATGTCGATGATGAGTAAATATAATATGGA 2182
DB 2058 TTCATGATTTATGTCATTTCAAAAGGAAATGATGAGAGAGATGATGATGATGAGG 2117
QY 2183 TCTGCAAACTACACAGAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 2242
DB 2118 TCTGCAAACTACACAGAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 2177
QY 2243 GCTATCAAACTACACAGAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 2296
DB 2178 GCTATCAAACTACACAGAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 2237
QY 2297 GCTATCAAACTACACAGAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 2356
DB 2238 GCTATCAAACTACACAGAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 2297
QY 2357 CCAGAAATGAGAGAGTGTGTCAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2416
DB 2298 CCAGAGAGCTTGAATGTCGAAGAGGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2357
QY 2417 TATCAAGCGAGACACTGAGACATGACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2476
DB 2358 TATGAGCAGCA---AGAGGTAACTGAAATGAAAGTCACTGATTAATAATATGCTGCTGAA 2414
QY 2477 GTCCGTAGTGAAGGAGATGTCACAGAGTCTGCTGCAAGTCTGCTGCTGCTGCTGCTGCTG 2540
DB 2415 GTTGATTCAGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2468

RESULT 8
US-10-078-770-119
; Sequence 119, Application US/10078770
; Publication No. US20030003471A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: eNAS Encoding Polypeptides
; FILE REFERENCE: 88-1365 US NA
; CURRENT APPLICATION NUMBER: US/10/078,770
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196

APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 9327
LENGTH: 261
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701102356H1
US-09-878-574-9327

Query Match 6.8%; Score 190.6; DB 10; Length 261;
Best Local Similarity 83.1%; Pred. No. 2.9e-48;
Matches 217; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 2089 TACAGCATATATAAGAGCTCAGGAGCCGAGAGCTTTTCATGATTATGTTTCATACAAAGAT 2148
DB 1 TTGAGATTATCAGAGAGCCCAAGAGCCGAGAGCTTCATGATTATGTTTCATACCAAGAT 60
QY 2149 GATGATTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2208
DB 61 GATGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 2209 GATGTTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2268
DB 121 GATGTTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 2269 CAGGAGCCGAGAGGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2328
DB 181 CAGGAGCCGAGAGGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 2329 TGGATGCTGCGAGAGTCAT 2349
DB 241 TGGATGCTTCATGATCTCTT 261

RESULT 12
US-09-878-574-9202
Sequence 9202, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 9202
LENGTH: 261
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701102205H1
US-09-878-574-9202

Query Match 6.5%; Score 181.2; DB 10; Length 263;
Best Local Similarity 83.2%; Pred. No. 2.4e-45;
Matches 218; Conservative 0; Mismatches 43; Indels 1; Gaps 1;
QY 645 GAAGTTCAAAATCTGGAGTACTTATACATCTTCGACAGACAGAGGATGAAG 704
DB 2 GAAGTCTAAATCTGGAGTACTTATACATCTTCGACAGACAGAGGATGAAG 61

QY 705 TTCTCTCTACCAAGATGCTCATATTCACAGACAAATTTGTTCTCAAAATCTCTCTGCTG 764
DB 62 TATCTCTGTACCAAGATGCTCATATTCGCTGCTGATATTTTGTACTAAATATCTCTGCTG 121
QY 765 GAGCAATTTACTATGAGGCTCACAGTCTGCTGGAGATGTTTTCGACCAATACCAAG 824
DB 122 GAGCAAGAAATTA-CAGGCTCATAGGTGTTGGAGATATATTTGATGCAATACCTGAG 180
QY 825 CAAAACACTTGATCTACATCATCTGCTGCTGTTTATACGAAATCTCTCTTAATAAGG 884
DB 181 CTAAACACTTCATATACATATCTGCTGCTGTTTATATGAAATCTCTCTGCTAAGG 240
QY 885 ACTCCAGGAGGCTCAAGCCAGG 906
DB 241 CTCTAGGAGGCTAAGCTGG 262

RESULT 13
US-09-770-445-688/c
Sequence 688, Application US/09770445
Patent No. US20020023281A1
GENERAL INFORMATION:
APPLICANT: Goriach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Kameoka, Joshua G.
APPLICANT: Pace, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 20240S (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 688
LENGTH: 833
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-445-688

Query Match 5.7%; Score 159.8; DB 10; Length 833;
Best Local Similarity 54.8%; Pred. No. 2.4e-38;
Matches 395; Conservative 0; Mismatches 302; Indels 24; Gaps 3;
QY 1885 GGATATACAGAGAGTGCATGCTGATATATATAGATGCTGACAAAGAGCAATGGA 1944
DB 833 GGGGAGCCCAAGAGCTGGGCTGTGCAAGAAATCTATATTCGACAGAGCAATGGA 774
QY 1945 AATGATGATAAAGATATTCGACAGCTCTCAAGCAATGAATATTATGAGATGCTG 2004
DB 773 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 714
QY 2005 GAATATCTGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2064
DB 713 CGATTACCTTAACCTTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 654
QY 2065 AACTGCAAGAAACAGAGAGCTGATATATGATATATATGAGAGCTTCAGAGAGAGAGAGCTTT 2124

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OM nucleic - nucleic search, using sw model

Run on: May 5, 2003, 02:25:32 ; Search time 153.263 Seconds
(without alignments)
5618.756 Million cell updates/sec

Title: US-09-817-869-2

Perfect score: 2808

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153348381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

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- 2: /cqn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cqn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cqn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cqn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cqn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2728.4	97.2	2834	1 US-08-471-251A-1	Sequence 1, Appli
2	1373.8	48.9	3040	1 US-08-446-794A-1	Sequence 1, Appli
3	1373.8	48.9	3040	1 US-08-750-007-2	Sequence 2, Appli
4	1373.8	48.9	3040	2 US-08-945-024-1	Sequence 1, Appli
5	1330.4	47.4	2804	1 US-08-446-794A-3	Sequence 3, Appli
6	150.4	5.4	2799	1 US-08-446-794A-5	Sequence 5, Appli
7	150.4	5.4	2799	1 US-08-750-007-4	Sequence 4, Appli
8	48.6	1.7	7218	1 US-08-232-463-14	Sequence 14, Appli
9	43.4	1.5	3108	3 US-08-968-752B-3	Sequence 3, Appli
10	43.4	1.5	3108	4 US-09-536-224-3	Sequence 3, Appli
11	43.4	1.5	3114	4 US-09-107-149-18	Sequence 18, Appli
12	43.4	1.5	3222	3 US-08-968-752B-1	Sequence 1, Appli
13	43.4	1.5	3222	4 US-09-536-224-1	Sequence 1, Appli
14	40	1.4	2799	3 US-08-968-752B-5	Sequence 5, Appli
15	40	1.4	2799	4 US-09-536-224-5	Sequence 5, Appli
16	36.4	1.3	4161	3 US-08-790-517-1	Sequence 1, Appli
17	36.4	1.3	4161	3 US-08-790-517-19	Sequence 19, Appli
18	36	1.3	3411	4 US-09-002-285-77	Sequence 77, Appli
19	45.8	1.3	152331	3 US-09-128-155-16	Sequence 16, Appli
20	35.8	1.3	176373	3 US-09-128-155-17	Sequence 17, Appli
21	44.4	1.2	3468	4 US-09-001-982-9	Sequence 9, Appli
22	44.4	1.2	3471	4 US-09-002-285-71	Sequence 71, Appli
23	34.4	1.2	4368	5 PCT-US95-04567-3	Sequence 3, Appli
24	34.2	1.2	9409	4 US-08-961-527-161	Sequence 161, Appl
25	34	1.2	3425	4 US-09-107-149-16	Sequence 16, Appli
26	34	1.2	11282	4 US-09-754-250-3	Sequence 3, Appli
27	33.8	1.2	651	4 US-09-341-444A-34	Sequence 34, Appli

28 33.4 1.2 5761 4 US-09-323-472A-1 Sequence 1, Appli
29 33.4 1.2 5761 4 US-09-323-472A-3 Sequence 3, Appli
30 33.4 1.2 5761 4 US-09-323-472A-11 Sequence 11, Appli
31 33.4 1.2 5762 4 US-09-323-472A-13 Sequence 13, Appli
32 33.2 1.2 4590 4 US-09-134-001C-1108 Sequence 1108, Appl
33 33 1.2 511 1 US-08-412-614-97 Sequence 97, Appl
34 33 1.2 511 1 US-08-412-614-98 Sequence 98, Appl
35 33 1.2 511 2 US-08-635-761-97 Sequence 97, Appl
36 33 1.2 511 2 US-08-635-761-98 Sequence 98, Appl
37 33 1.2 511 4 US-09-412-520-97 Sequence 97, Appl
38 33 1.2 511 4 US-09-312-520-98 Sequence 98, Appl
39 33 1.2 3388 4 US-09-141-206-1 Sequence 1, Appli
40 32.8 1.2 2128 2 US-08-415-593-39 Sequence 39, Appli
41 32.8 1.2 3201 3 US-08-556-419-11 Sequence 11, Appli
42 32.8 1.2 3708 3 US-08-556-419-10 Sequence 10, Appli
43 32.6 1.2 654 4 US-09-385-982-346 Sequence 346, Appl
44 32.6 1.2 43360 4 US-09-453-702B-206 Sequence 206, Appl
45 32.6 1.2 45325 4 US-09-453-702B-251 Sequence 261, Appl

ALIGNMENTS

RESULT 1
US-08-471-251A-1
: Sequence 1, Application US/08471251A
: Patent No. 5670366
: GENERAL INFORMATION:
: APPLICANT: Wang, Xuebin
: TITLE OF INVENTION: RECOMBINANT DNA SEQUENCES ENCODING
: TITLE OF INVENTION: PHOSPHOLIPASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
: ADDRESSEE: Collins
: STREET: 2405 Grand Boulevard, Suite 400
: CITY: Kansas City
: STATE: Missouri
: COUNTRY: U.S.A.
: ZIP: 64108
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/471,251A
: FILING DATE: June 6, 1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Collins, John M.
: REGISTRATION NUMBER: 26262
: REFERENCE/DOCKET NUMBER: 23703
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (816) 474-9050
: TELEFAX: (816) 474-9057
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2834 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: circular
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHEetical: NO
: ANTI-SENSE: NO
US-08-471-251A-1

Query Match 97.2% Score 2728.4; DB 1; Length 2834;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2785; Conservative 0; Mismatches 21; Indels 4; Gaps 4;
QY 1 CTTGTTTCACATTCTGTCTACTTTTACATTAACAGTCATACAAATTAATTTATTTGAT 60
|||||

ATTORNEY/AGENT INFORMATION:
NAME: Giotto, Gregory J.
REGISTRATION NUMBER: 42,028
REFERENCE/DOCKET NUMBER: ONYX2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4222 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 1..4222
US-09-868-752B-1

Query Match 1.5% Score 43.4; DB 3; Length 4222;
Best Local Similarity 62.4%; Pred. No. 0.0073;
Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2127 TGATTATGTCATACAAAGATGATGTCGATGATGATGATGATGATGATGATGATGATG 2186
DB 2675 TTATCTATGTCACAGCAAGTTGTAATGCTGATGATACACTGTTATTATGTCCTG 2734

QY 2187 CCAACATCAACGACATCAATCATGTCGTGTACAGACTCCGAAATAGC 2235
DB 2735 CCAACATAAATGACGACGATCTGTGGAAAGGCTGACATGCAATGCG 2783

RESULT 13

US-09-536-224-1
Sequence 1, Application US/09536224
Patent No. 6379665

GENERAL INFORMATION:

APPLICANT: Frohman, Michael A.
APPLICANT: Morris, Andrew
TITLE OF INVENTION: No. 6379665e1 Phospholipase D Polypeptide and
NUMBER OF SEQUENCES: 8
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 4031 Research Drive
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94806

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,224
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/968,752
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Giotto, Gregory J.
REGISTRATION NUMBER: 42,028
REFERENCE/DOCKET NUMBER: ONYX2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4222 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4222
US-09-536-224-1

Query Match 1.5% Score 43.4; DB 4; Length 4222;
Best Local Similarity 62.4%; Pred. No. 0.0073;
Matches 68; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2127 TGATTATGTCATACAAAGATGATGTCGATGATGATGATGATGATGATGATGATGATG 2186
DB 2675 TTATCTATGTCACAGCAAGTTGTAATGCTGATGATACACTGTTATTATGTCCTG 2734

QY 2187 CCAACATCAACGACATCAATCATGTCGTGTACAGACTCCGAAATAGC 2235
DB 2735 CCAACATAAATGACGACGATCTGTGGAAAGGCTGACATGCAATGCG 2783

RESULT 14

US-08-968-752B-5
Sequence 5, Application US/08968752B
Patent No. 6043073

GENERAL INFORMATION:

APPLICANT: Frohman, Michael A.
APPLICANT: Morris, Andrew
TITLE OF INVENTION: No. 6043073e1 Phospholipase D Polypeptide and
NUMBER OF SEQUENCES: 8
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 4031 Research Drive
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94806

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,752B
FILING DATE: 13 Aug 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,469
FILING DATE: 05 SEP 1996

ATTORNEY/AGENT INFORMATION:

NAME: Giotto, Gregory J.
REGISTRATION NUMBER: 42,028
REFERENCE/DOCKET NUMBER: ONYX2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 2799 base pairs
TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2799

US-08-968-752B-5

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2003, 21:54:51 ; Search time 730.346 Seconds
(without alignments)
8658.379 Million cell updates/sec

Title: US-09-817-869-2
Perfect score: 2808
Sequence: 1 cttgctttcacattctctat.....catgctttttctacaaac 2808

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002.*
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6: /SID52/qcdata/geneseq/geneseq-emb1/NA1985.DAT.*
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15: /SID52/qcdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SID52/qcdata/geneseq/geneseq-emb1/NA1995.DAT.*
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19: /SID52/qcdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID52/qcdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID52/qcdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID52/qcdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID52/qcdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/qcdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2728.4	97.2	2834	18	AA188222
2	1373.8	48.9	3040	16	AA086783
3	1373.8	48.9	3040	17	AA142853
4	1373.8	48.9	3040	18	AA185509
5	1164.8	41.5	2708	16	AA086784
6	539.8	19.2	1062	24	AA08376
7	317.4	11.3	3216	21	AA042946
8	252.8	9.0	1997	21	AA047118
9	232	8.3	641	22	AAH50934

Castor bean phosph
DNA encoding Phosp
Phospholipase D pr
Phospholipase D en
DNA encoding Phosp
Arabidopsis thalia
Arabidopsis thalia
Lipid degradation

10	232	8.3	641	22	AAH56941
11	220.8	7.9	551	22	AAH50935
12	220.8	7.9	551	22	AAH56942
13	217.6	7.7	1173	22	AAH21721
14	181.2	6.5	639	22	AAH50936
15	181.2	6.5	639	22	AAH56943
16	159.8	5.7	833	24	AAH98920
17	150.4	5.4	2799	16	AA086785
18	150.4	5.4	2799	17	AA142854
19	108.8	3.9	452	24	AAH94878
20	51.6	1.8	1468	24	AA048885
21	44.6	1.6	1070	24	AAH94866
22	44	1.6	224	24	AAH74623
23	43.4	1.5	667	21	AAH21983
24	43.4	1.5	8108	19	AAV20869
25	43.4	1.5	3114	21	AAZ4971
26	43.4	1.5	3114	22	AAH47447
27	43.4	1.5	3222	19	AAV21867
28	43.4	1.5	3495	19	AAV20870
29	43.4	1.5	3609	19	AAV20868
30	43.4	1.5	3609	24	AAH59518
31	43.4	1.5	3620	22	AAH98437
32	43.4	1.5	3703	23	AAH83114
33	43.4	1.5	4434	23	AAH19571
34	43.4	1.5	4497	23	AAH19569
35	43.4	1.5	14245	23	AAH10348
36	43.4	1.5	15238	23	AAH19570
37	43.4	1.5	15243	23	AAH19568
38	42	1.5	1664976	19	AAV21209
39	40	1.4	2799	19	AAV20871
40	40	1.4	3374	19	AAV20872
41	38.6	1.4	103929	21	AAV22287
42	37.6	1.3	5312	24	AAH32197
43	37	1.3	5303	24	AAH32871
44	36.6	1.3	191	22	AAH16388
45	36.6	1.3	191	22	AA122902

ALIGNMENTS

RESULT 1
ID AAT88222 standard; cDNA to mRNA: 2834 BP.
AC AAT88222:
XX
DT 19-JAN-1998 (first entry)
DE Castor bean phospholipase D cDNA.

Castor bean: phospholipase D; hydrolysis: phospholipid: production;
phosphatidic acid; transphosphatidyl derivative; endosperm: ds.

OS Ricinus communis.
FH Key Location/Qualifiers
FT CDS 172..2598
FT /*taq a
FT /product : phospholipase_D
XX
PN US5670366-A.
XX
PD 23-SEP-1997.
XX
PF 06-JUN-1995; 95US-0471251.
XX
PR 06-JUN-1995; 95US-0471251.
XX
PA (UNIV) UNIV KANSAS STATE RES FOUND.
XX
PI Wang X;
XX

P patens lipid met.
Lipid degradation
P patens lipid met.
Tobacco phospholip
Lipid degradation
P patens lipid met.
Arabidopsis thalia
DNA encoding Phosp
Phospholipase D ge
Arabidopsis thalia
Altilia plastocyan
Arabidopsis thalia
Corn tassei-deri
Aspergillus oryzae
Human phospholip
Human phosphatidyl
Human phosphatidyl
Human phospholip
Human phospholip
Human phospholip
Human phospholip
Human EST-derived
DNA encoding novel
Protophila melano
Protophila melano
Protophila melano
Protophila melano
Protophila melano
Methanococcus jann
Murine phospholip
Murine phospholip
RA' containing rep
Human immune syste
Human immune syste
Human brain expres
Probe #12835 for q

DR WPI; 1997-479462/44.
DR P-PSDB; AAW32911.

DR P-PSIB; AAW32411.

recombinant Ricinus communis phospholipase D gene - which hydrolyses phospholipid(s) to produce phosphatidic acid and trans:phosphatidyl derivatives

[illegible]

PS Claim 6: Columns 11-14: 14pp: English.

XX The present sequence encodes castor bean phospholipase D (PLD),
CC which hydrolyses phospholipids to produce phosphatidic acid and
CC transphosphatidyl derivatives.

A lambda zap cDNA library from castor bean endosperm was screened with P1D cDNA specific probes. Clones that hybridised with both probes were excised *in vivo* with helper phage R344 in pBluescript SK(-). Both ends of the inserts were sequenced. The deduced amino acid sequence from 1 clone matched the amino-terminal sequence of purified Ricinus communis P1D.

XX
XX
X

SQ Sequence 2834 BP; 815 A; 550 C; 668 G; 801 T; 0 other;

Query Match

Year of publication	Author	Year of publication	Author
1990	Alvarado	1996	Ward
1991	Stor	1997	Ward
1992	Stor	1998	Ward
1993	Stor	1999	Ward
1994	Stor	2000	Ward
1995	Stor	2001	Ward
1996	Stor	2002	Ward
1997	Stor	2003	Ward
1998	Stor	2004	Ward
1999	Stor	2005	Ward
2000	Stor	2006	Ward
2001	Stor	2007	Ward
2002	Stor	2008	Ward
2003	Stor	2009	Ward
2004	Stor	2010	Ward
2005	Stor	2011	Ward
2006	Stor	2012	Ward
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2013	Stor	2019	Ward
2014	Stor	2020	Ward
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2019	Stor	2025	Ward
2020	Stor	2026	Ward
2021	Stor	2027	Ward
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2023	Stor	2029	Ward
2024	Stor	2030	Ward
2025	Stor	2031	Ward
2026	Stor	2032	Ward
2027	Stor	2033	Ward
2028	Stor	2034	Ward
2029	Stor	2035	Ward
2030	Stor	2036	Ward
2031	Stor	2037	Ward
2032	Stor	2038	Ward
2033	Stor	2039	Ward
2034	Stor	2040	Ward
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2073	Stor	2079	Ward
2074	Stor	2080	Ward
2075	Stor	2081	Ward
2076	Stor	2082	Ward
2077	Stor	2083	Ward
2078	Stor	2084	Ward
2079	Stor	2085	Ward
2080	Stor	2086	Ward
2081	Stor	2087	Ward
2082	Stor	2088	Ward
2083	Stor	2089	Ward

Matches	2785	Conservative	0	Mismatches	21	Indels	4	Gaps	4
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[illegible]

Db	1807	CCCAAGGAAC	TTTCACTCAAGATCTTACGAGATTCGGCAGGGAGAGGTTCACTGTT	1866
QY	1859	TACATTGTGTTTCCAAATGTCGCCAGAGG	GTATACGAGAGTGCATCAGTTCAGGCTATA	1918
Db	1867	TAATGTGTTGTTCCAAATGTGGCCAGAGG	GTATACGAGAGTGCATCAGTTCAGGCTATA	1926
QY	1919	TTAGATTGCACAAAGACACAAATG	CAATGATGATTAAGAAATATTGTGCAGCTCTCAAA	1978
Db	1927	TTAGATTGCACAAAGAGACAAATG	CAATGATGATTAAGAAATATTGTGCAGGCTCTCAAA	1986
QY	1979	GGCAATGGAAATTATTGAGGATGCTCGGA	AACTATCTGCATTTCTGCCCTTGGTAAACCGC	2038
Db	1987	GGCAATGGAAATTATTGAGGATGCTCGGA	AACTATCTGCATTTCTGCCCTTGGTAAACCGC	2046
QY	2039	GAAGTGAAGACAGTGGTCAATATGAAC	CTCGAGAAAACAGAGCGCTGATACAGACTAT	2098
Db	2047	GAAGTGAAGACAGTGGTCAATATGAAC	CTCGAGAAAACAGAGCGCTGATACAGACTAT	2106
QY	2099	ATAAGAGCTCAGAGGCGCAGAGCTTT	TCATGATTTATGTTCTACAAAGATGATGATTGC	2158
Db	2107	ATAAGAGCTCAGAGGCGCAGAGCTTT	TCATGATTTATGTTCTACAAAGATGATGATTGC	2166
QY	2159	GATGATGACTACATTATAATTGGATCT	GCCCAACATCAACAGAGATCAATGGATGGTCT	2218
Db	2167	GATGATGACTACATTATAATTGGATCT	GCCCAACATCAACAGAGATCAATGGATGGTCT	2226
QY	2219	AGAGACTCCGAATAGCCATGGAGCCCT	ATCAATCAATCATCTGTCAAATCAGCAGCCAA	2278
Db	2227	AGAGACTCCGAATAGCCATGGAGCCCT	ATCAACCAATCATCTGTCAAATCAGCAGCCAA	2286
QY	2279	GCACGAGGTCAGATGCATGGTTTCGGT	ATGTCATTATGGTACGAAACACCTTGGCATGCTC	2338
Db	2287	GCACGAGGTCAGATGCATGGTTTCGGT	ATGTCATTATGGTACGAAACACCTTGGCATGCTC	2346
QY	2339	GAGGAGTCATTCCCTTAATCCAGAAAGT	GAGGAGTGTGTGCAAGAAAGTGAACAGATGGCA	2398
Db	2347	GAGGAGTCATTCCCTTAATCCAGAAAGT	GAGGAGTGTGTGCAAGAAAGTGAACAGATGGCA	2406
QY	2399	GAATAATTTGGATCTCTATTCAAGCC	CAGACACTGCAACATGACCTACCTGGTCAATTG	2458
Db	2407	GAATAATTTGGATCTCTATTCAAGCC	CAGACACTGCAACATGACCTACCTGGTCAATTG	2466
QY	2459	CTCCGGTATCTTATTGGGTGCGCTAGT	GAGGAGATGTGCAAGAAAGTGCCTGGAACCGAG	2518
Db	2467	CTCCGGTATCTTATTGGGTGCGCTAGT	GAGGAGATGTGCAAGAAAGTGCCTGGAACCGAG	2526
QY	2519	TTTTCCCTCGACAGGAAGCTCGTGTCT	GTAGTGCTAAATCCGATTACCTTCCTCCCATC	2578
Db	2527	TTTTCCCTCGACAGGAAGCTCGTGTCT	GTAGTGCTAAATCCGATTACCTTCCTCCCATC	2586
QY	2579	CTGACAACTTAATGGAAGCTTAAGCAG	ATTCGGAAGAAATTAACCTGGCTTGGCAGCCCAT	2638
Db	2587	CTGACAACTTAATGGAAGCTTAAGCAG	ATTCGGAAGAAATTAACCTGGCTTGGCAGCCCAT	2646
QY	2639	TATGTTACTAGTTGTAGCCAGCAAAAT	TAATCATGCTATGCCATTCTATCCATATGTTTT	2698
Db	2647	TATGTTACTAGTTGTAGCCAGCAAAAT	TAATCATGCTATGCCATTCTATCCATATGTTTT	2706
QY	2699	TGTGCCAGGATTTGGGATATCAGGATTT	GCAGATGTCACCTGCTGTGTGGTGTGATG	2758
Db	2707	TGTGCCAGGATTTGGGATATCAGGATTT	GCAGATGTCACCTGCTGTGTGGTGTGATG	2766
QY	2759	CTGTCTATGTTGAACCTTGTCTTATCT	TAATCCATGCTCTTTTCTACAAAAC	2808
Db	2767	CTGTCTATGTTGAACCTTGTCTTATCT	TAATCCATGCTCTTTTCTACAAAAC	2816

RESULT 2
AAQ86783
ID AAQ8
XX
AC AAQ8

XX	01-MAR-1996	(first entry)	
XX	DT		
XX	DE	DNA encoding Phospholipase D.	
XX	XX		
KW	phospholipase D: measurement; reagent; phospholipid level; ss.		
XX	OS	oryza sativa.	
XX	XX		
KY	Key	Location/Qualifiers	
XX	FT	182..2620	
FT	/tag= a		
FT	/product= phospholipase D		
XX	XX		
DN	WO9509234-A1.		
XX	XX		
PD	06-APR-1995.		
XX	XX		
PF	30-SEP-1994;	54WO-JP01627.	
XX	XX		
PR	30-SEP-1993;	54JP-0267884.	
XX	XX	(NLSB) JAPAN TOHACCO INC.	
PA	XX		
PI	Morioka S, Ueki J;		
XX	XX		
DR	WPI: 1995-147433/19.		
DR	P-PSDR: AAR72797.		
XX	XX		
PT	Cloned DNA coding plant derived phospholipase D - controls		
PT	expression of plant derived PLD gene		
XX	XX		
PS	Claim 7: Page 14-19; 41pp; Japanese.		
XX	XX		
CC	The DNA encodes a plant derived phospholipase D (PLD). The PLD is		
CC	useful for measuring phospholipid levels and for producing derivs.		
CC	by e.g. base exchange reactions. DNA controlling the expression of		
CC	the plant derived PLD is also claimed and shown in AA086785.		
XX	Sequence 3040 BP; 784 A; 724 C; 783 G; 749 T; 0 other;		
XX	Sequence 3040 BP; 784 A; 724 C; 783 G; 749 T; 0 other;		

RESULT 2
AAQ86783
ID AAQ86783 standard; cDNA to mRNA; 3040 BP.
XX
AC AAQ86783;

XX	Key	Location/Qualifiers
FH	CDS	181..2620
FT	/taq*	a
FT	/product=	phospholipase D
XX	W096.40510-AL.	
XX	PD	03-OCT-1996.
XX	XX	28-MAR-1996.; 96WO-JP00812..
XX	PR	29-MAR-1995.; 95JP-0096126..
XX	PA	(NLSB) JAPAN TOBACCO INC.
XX	PI	Morioka S., Ueki J;
XX	DR	WPI; 1996-455357/45.
XX	DR	P-PSDB; AAW06134.
PT	PT	Promoter DNA sequence derived from rice - used to increase expression of foreign genes in transformed hosts
XX	XX	Disclosure; Page 14-20; 29pp; Japanese.
CC	CC	This sequence represents the coding sequence for the rice phospholipase D gene (PLD). The promoter for the PLD gene was isolated using the primers shown in AAT42857 and AAT42588. The promoters (see AAT42851 and AAT42852) are efficient promoters for greatly increasing the expression of foreign genes in transformant rice and other plants.
XX	XX	Sequence 3040 bp; 784 A; 724 C; 783 G; 749 T; 0 other;
SQ	Query Match	48.9%; Score 1373.8; DB 17; Length 3040;
	Best Local Similarity	74.0%; Pred.No. 0;
	Matches 1734; Conservative	0; Mismatches 612; Indels 3; Gaps 1;
QY	226	CAGCGGAGGTGGTCCCCACTTCCTTTGGTAGCTTGTTGAATAATTGAGGACAGCTGGG 285
Db	259	CAGCGAAGGCCGCCCAAGTTTCATCCGCAAGTTTGTGGAGGGATTGAGGCACCTGTGGG 318
QY	286	TTTTGGCAAGGAGTAGTAACCTCTATGCACTATTGACCTAGAAAAGGCTAGAGTTGG 345
Db	319	TGTGGCAAGGCGCCACCAGGTGATTTCTACCATTTGATCTGGAGAAAGCTCGTGTAGG 378
QY	346	GAGSACTAGAATACTGAAAAACAACATCCAAACCCAGGTGCTATGAGTCCTTTCAAGT 405
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QY	406	TTATTGGCTCCTCAGGCTTCAAATGTAATATTCACAGTCAAGGATCAATATCTTATGG 465
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QY 863 ACTGAATCTGCTTAATAAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGATATATCTGCT 922
DB 790 CATAGATTAAGCTTGTAG 846
QY 923 GATCAATCTGCTTAAG 982
DB 847 GGGGAATTCCTCAATCAATATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 906
QY 983 CACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1036
DB 907 GATAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
QY 1037 CAGAGAGCTGAGCAATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
DB 967 CAGAGAGCTAGAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1026
QY 1097 GCTGATGATGCTGAG 1156
DB 1027 GCGAGAGCTGAG 1086
QY 1157 CAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
DB 1087 ATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 1194 GCGAGAGCTGAG 1252
DB 1147 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
QY 1254 AGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1312
DB 1207 GCTGATGAG 1266
QY 1413 TTTCATGAG 1372
DB 1267 TTTCATGAG 1317
QY 1474 CATGAG 1432
DB 1418 CAG 1377
QY 1444 CAG 1447
DB 1478 CAG 1437
QY 1448 CAG 1507
DB 1448 CAG 1447
QY 1508 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1525
DB 1498 TTTAAATTCGAG 1557
QY 1526 GATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1576
DB 1558 TCTAAAG 1617
QY 1577 GCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1646
DB 1618 TCTGAG 1677
QY 1647 AAG 1696
DB 1678 AAG 1747

QY 1697 AAG 1756
DB 1748 CAG 1797
QY 1757 GAG 1806
DB 1798 CAG 1845
QY 1817 AAG 1876
DB 1846 AAG 1905
QY 1877 GAG 1946
DB 1906 TGGAG 1965
QY 1937 AAG 1996
DB 1966 AAG 2025
QY 1997 GAG 2056
DB 2026 CAG 2085
QY 2057 GAG 2116
DB 2086 AAG 2140
QY 2117 AAG 2176
DB 2141 CAG 2190
QY 2177 AAG 2246
DB 2191 AAG 2250
QY 2237 AAG 2290
DB 2251 AAG 2340
QY 2291 AAG 2350
DB 2311 GAG 2370
QY 2351 CTTAAG 2410
DB 2371 GAG 2440
QY 2411 GAG 2470
DB 2431 AAG 2487
QY 2471 AAG 2540
DB 2488 CTTAAG 2547
QY 2531 AAG 2590
DB 2548 GAG 2607
QY 2591 GAG 2654
DB 2608 GAG 2640

RESIDUE 8
AA-47118
ID AA-47118 standard; IMA: 1997 RP.
XX AA-47118;
XX AA-47118;
ID 18-001-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52628.
XX DE
XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

XX OS Arabidopsis thaliana.
XX PN EP103405-A2.
XX PD 06-SEP-2000.
XX XX

XX PF 25-FEB-2000; 2000EP-0301439.
XX XX
XX 25-FEB-1999; 990S-0121825.
PR 05-MAR-1999; 990S-0123180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
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PR 21-JUL-1999; 990S-0144814.
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PR 27-JUL-1999; 990S-0145913.
PR 27-JUL-1999; 990S-0145918.
PR 27-JUL-1999; 990S-0145919.
PR 28-JUL-1999; 990S-0145951.
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PR 04-AUG-1999; 990S-0147302.
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PR 18-AUG-1999; 990S-0149426.
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PR 20-AUG-1999; 990S-0149723.
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PR 23-AUG-1999; 990S-0149930.
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PR 26-AUG-1999; 990S-0150884.
PR 27-AUG-1999; 990S-0151065.
PR 27-AUG-1999; 990S-0151066.

KW rice; barley; soybean; peanut; cotton; rapeseed; canola; manihot;
 KW pepper; sunflower; tagetes; potato; tobacco; eqplant; tomato; Vicia;
 KW pea; alfalfa; coffee; cacao; tea; Salix; oil palm; coconut;
 KW perennial grass; forage crop; ss.
 XX Physcomitrella patens.
 XX WO200138484-A2.
 XX 31-MAY-2001.
 XX 22-NOV-2000; 2000WO-EPI1615.
 XX 25-NOV-1999; 99WO-EP09108.
 XX (BADI) BASF PLANT SCI GMBH.
 XX Lerchl J, Renz A, Ehrhardt T, Reindl A, Cirpus P, Bischoff F;
 PI Frank M, Freund A, Duwenig E, Schmidt R, Reski R;
 XX WPI: 2001-367669/38.
 XX Nucleic acids encoding lipid metabolism related proteins from
 PT Physcomitrella patens useful to produce fine chemicals in modified
 PT organisms, particularly polyunsaturated fatty acids in oilseed plants -
 XX Claim 7: Page 98; 120pp; English.
 XX The present invention describes isolated nucleic acid sequences which
 CC encode lipid metabolism related proteins (LMP). The LMP nucleic acids
 CC can be used to modify lipids and fatty acids, cofactors and enzymes in
 CC microorganisms and plants, particularly to produce polyunsaturated fatty
 CC acids, and are especially useful in oilseed plants. The nucleic acids
 CC may also confer biotic or abiotic stress tolerance, particularly to
 CC maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut,
 CC cotton, rapeseed, canola, manihot, pepper, sunflower, tagetes, potato,
 CC tobacco, eqplant, tomato, Vicia species, pea, alfalfa, coffee, cacao,
 CC tea, Salix species, oil palm, coconut, perennial grasses and forage
 CC crops. AAH50878 to AAH50882 represent primers used in the exemplification
 CC of the present invention. AAH50883 to AAH50968 represents LMP nucleotide
 CC sequences, and AAG80843 to AAG80928 represent LMP protein sequences,
 CC given in the present invention.
 XX Sequence 639 BP; 145 A; 144 C; 189 G; 160 T; 1 other;
 SQ

Query Match 6.5%; Score 181.2; DB 22; Length 639;
 Best Local Similarity 59.8%; Pred. No. 3.1e-43;
 Matches 406; Conservative 0; Mismatches 219; Indels 54; Gaps 4;

QY 1209 GGAGAAATGTCAGTTTGTGGGGTCTCGACCTCTGTGATGGAGATATGATTCGCCCAT 1268
 DB 12 GGAGCTTGTAAAGCTTGTGGGAGACTGGACCTCTGTGACGCCCTATGACAAACAGT 71
 QY 1269 TCCATCCCTTTTCAGACACTGATTCGGCAGCACCATGATGATTTTCATCAGCCCACT 1328
 DB 72 TCCATCTCTGTCGGCAGCTTTGATACGCTCAGCTCGGGATTTCCATCA---AGTGT 128
 QY 1329 TTGCTGGTGTCTCAATTGAAAAGGTTGTCACAGAACCTTGGCATGACATCCACTCCA 1388
 DB 129 TTACTGAGGCTCGTGCAATGTGGCGACCTGTGAGCGNGGACGACATCCACTCTA 188
 QY 1389 GACTTGAAGCAACAATTCGTTGGATGTTTGTGTTTAAATTTTGAACAGACATGGAGAAAGC 1448
 DB 189 AGTTGAAGGTCCTGTTGCTGGGATGTTCTCAGCAATTTTGAAGAGATGAGAAAAAC 248
 QY 1449 AAGTGTGAAGACTCTCTATTCAGTCAGACAGACTAGAGATGTTATCATTCGCCCAT 1508
 DB 249 AGGCTG-----GCGGCGGGGAGTCTTTTGGCCATCCGAGATCTTGATCTCTCGTG 302
 QY 1509 CTCCTGTTATGATGCTGATGACTTTGAGGATGGATGTCAGTGTGTTAGATCCATTC 1568
 DB 503 ATCTGTTACAGTAGAGAGATGACAGGAGACCTGGAATGTCAGGTTTTCGCTCAATG 362

QY 1569 ATGGTGGAGCTGCATTTGGTTTTCCTGTGAGACACCTGAGATGGCGACAGAGCTGGCTTG 1628
 DB 363 ACCAGAGGCTG-----CAATAAAGGTTTG 389
 QY 1629 TCAGTGGAAAGGATAACATCATTTGACCGAAGTATTCAGGATGCTTATATCTATGCGATTC 1688
 DB 390 TGAGTGGGAAAAATATCTCAATTGACCGAGTATTCAGCATGCGATGACATCAATGCAATA 449
 QY 1689 GAAGGCGCAAGAAATTTATTTATATGAAAAACAGTATTTCTTGAAGTCTTTGGTT 1748
 DB 450 GAGCTGCGGAAACTTCATTTATATGAGAAATCATAGTCTTTGGAGAGCATTTTGGT 509
 QY 1749 GGAGTCTCTGATGATTAAGCTGAGATATTAATGATGTCGATCTAATACATTAAGCAAC 1808
 DB 510 GCGAAGCGAAGA-----AGGAGCGCGGGCATTCACCTTATCCCAATGGAGCT 557
 QY 1809 TTTCACCTCAAGATACATTCAGCAATTCGCGCAGGAGGAGGATGATGATGATGTTG 1868
 DB 558 TTGTCGCGAAGATGCTGAGCAAAATGGAAGCTGGGAGAGGCTTGGGCTGATGTTGA 617
 QY 1869 TTCCAATGTGGCGAGAGGG 1887
 DB 618 TACCGATGATCTGGAAGG 636
 RESULT 15
 AAH56943
 ID AAH56943 standard: cDNA; 639 BP.
 XX AC AAH56943;
 XX DT 06-SEP-2001 (first entry)
 XX P patens lipid metabolism related protein coding sequence #70.
 XX Moss: LMRP; lipid metabolism related protein; polyunsaturated fatty acid;
 KW fine chemical; transgenic plant; ss.
 OS Physcomitrella patens.
 XX WO200138541-A1.
 XX 31-MAY-2001.
 XX 25-NOV-1999; 99WO-EP09108.
 PR 25-NOV-1999; 99WO-EP09108.
 XX (BADI) BASF PLANT SCI GMBH.
 XX Lerchl J, Renz A, Ehrhardt T, Reindl A, Cirpus P, Bischoff F;
 PI Frank M, Freund A, Duwenig E, Schmidt R, Reski R;
 XX WPI: 2001-381293/40.
 DR New isolated nucleic acid molecule encoding Lipid Metabolism Related
 PT Proteins useful in the production of fine chemicals -
 XX Claim 7: Page 95-96; 113pp; English.
 CC The present invention provides the protein and coding sequences of a
 CC number of moss lipid metabolism related proteins (LMRPs). The moss
 CC Physcomitrella patens is one of the few plants able to produce
 CC polyunsaturated fatty acids, and the sequences can be used to create
 CC transgenic plants also capable of producing them. They can also be used
 CC to identify the presence of P. patens and in the production of fine
 CC chemicals. The present sequence is one of the cDNAs of the invention.
 XX Sequence 639 BP; 145 A; 144 C; 189 G; 160 T; 1 other;
 SQ

Query Match 6.5%; Score 181.2; DB 22; Length 639;
 Best Local Similarity 59.8%; Pred. No. 3.1e-43;
 Matches 406; Conservative 0; Mismatches 219; Indels 54; Gaps 4;

QY	1209	GGAGAAATGTCACATTTTGTGTGGGGTCTCGAGCTCTGTGATATGGAGATATGATATTCACAT	1268
DB	12	GGAGGCTGTGAAGCTTTTGTGGAGACATCGAGACCTGTGTGCAAGGCGGTATGCAAACTCAGT	71
QY	1269	TCCATTCCTTTTCACAGACACTTGGATTGGATCGGACATCATCATCATATTTTCATACGCGCAACT	1328
DB	72	TCCACTCTCTGTTCGCACATCTGTGATAGGGTTCACAGTCGGGATTTCCATCA - AGTGT	128
QY	1429	TTGCTGCTGCTTCAATTGAAAAAGGTGGTCCAAAGAGAAGCTTGGATCGATCATATCCACTCCA	1488
DB	129	TTACTTGAAGTTCGGTGGGAATGTGGGGAGCTGGTGGAGCGGNGGACGATATTCATCTCTA	188
QY	1389	GACTTGAAGGACCAATTCGCTGGGAGATTTTGTAAATTTTCACGACAGATGAGAAAGC	1448
DB	189	AGTTCGAAGATCTCTGTGGTGGATGTTCTTCACAAATTTTCAGACAGATGAGAAAAAC	248
QY	1449	AAGTGTTAAAGACCTGCTTCATTCACCTCAGACAACTAGAAATGTTATATTCGCCCCAT	1508
DB	249	AGGCTGG-----GGGGCGGGGAGCTTTTGGCATCGGAGATCTTGTATCTCTGGT	402
QY	1509	CTNTCTGTATATCTGATGACTTTCAGCATGCAATTCAGCAATGCAATGTCAGTTGTTAGATCCATTG	1568
DB	403	ATGCTGTTACACATGACGAGAGATCGACAGATCTGAAATGCGAGCTGTTGGTCAAATTG	362
QY	1569	ATGCTGCACTGCAATTTGGTTTCTCGAGACATCTGGAAGATGGGCGACAGCTGGGTTG	1628
DB	463	ACGAGAGAGCTG-----CAATAAAGGTTTGG	489
QY	1629	TCACTTAAAGCAAAACATCATGAGCGCAAGCATTTTCAGCATCTTATATCATGCTATTG	1688
DB	490	TGACTGGAAAAATCATCAATGACCGAGATATCACATGCTATCATATGCAATTA	449
QY	1689	GAAGGGCAAGAAATTTATTATATGAAAAATCAGTATTTCCTTGGAAATTTCTTTGGGTT	1748
DB	450	GAGCTGGCGCAAACTTCATTTATATCGAATTCAGTACTTCTTGGGAGCAGATTTTGGCT	509
QY	1749	GGACTTCTATGATTAAGCTTCAGCATATTAATGCACTGCAATCTAAATCAATCAAGCAAC	1808
DB	510	GGGAAGCGAAGA-----ACGAGCGGGGGCAATCAAGCTTATCCCATGAGGC	567
QY	1809	TTTCATCTCAAGATATCATAGCAATTCGGGAGGGCAGAGCTTCACCTTTTACATCTTG	1868
DB	558	TTGTCGCAAGATGTCGACAAATCGAAGCTGAGACAGCTTCGCGCTGTATGTTCTGA	617
QY	1869	TTTCAATGTGGGCAGAGG	1887
DB	618	TATCGAATGATATCGTGAAGG	646

Search completed: May 5, 2003, 02:41:00
Job time : 747.346 secs

GenCore version 5.1.5
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GM nucleic - nucleic search, using sw model

Run on: May 4, 2003, 21:56:05 ; Search time 8380.21 Seconds
(without alignments)
9751.626 Million cell updates/sec

Title: US-09-817-869-2

Perfect score: 2808

Sequence: 1 cttcgtttcacattctctgt.....catgtctttttctacaaaac 2808

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_em.*
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- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
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- 40: em_htg_mus.*
- 41: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2808	100.0	2808	8	RCGPLD	L34686 Ricinus com
2	2728.4	97.2	2834	6	166478	166478 Sequence 1
3	1901.4	67.7	5676	8	RCU72693	072693 Ricinus com
4	1652.8	58.9	2911	8	V0092656	092656 Nicotiana t
5	1589.2	56.6	2723	8	NT284822	284822 Nicotiana t
6	1589.2	56.6	2697	8	AY013252	AY013252 lycopersi
7	1574.8	56.1	2427	8	AF201661	AF201661 lycopersi
8	1509	53.7	2859	8	P0096438	096438 Pinguicula
9	1426.8	50.8	2674	8	CPL134001	AJ133001 Craterost
10	1415.8	50.4	2794	8	AT036381	U46481 Arabidopsis
11	1412.2	50.3	2743	8	B0085482	085482 Brassica ol
12	1411.4	50.3	2702	8	AF090444	AF090444 Brassica
13	1405	50.0	2848	8	AF154425	AF154425 lycopersi
14	1397.2	49.8	2793	8	AF090445	AF090445 Brassica
15	1380.4	49.2	81370	8	AB017071	AB017071 Arabidops
16	1373.8	48.9	2390	8	RICPHD2	D73411 oryza sativ
17	1373.8	48.9	3040	6	AR005011	AR005011 Sequence
18	1373.8	48.9	3040	6	AR037062	AR037062 Sequence
19	1373.8	48.9	3040	6	AR082616	AR082616 Sequence
20	1360.6	48.5	2662	8	CPL134000	AJ133000 Craterost
21	1345	47.9	11737	8	F6D8	AC008016 Arabidops
22	1340.4	47.7	2829	8	AY013253	AY013253 lycopersi
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24	1330.4	47.4	2804	6	AR005012	AR005012 Sequence
25	1276.8	45.5	2903	8	AY013254	AY013254 lycopersi
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27	1125.8	40.1	135295	8	AP003282	AP003282 oryza sat
28	1124.2	40.0	5871	8	AR001920	AR001920 oryza sat
29	1115	39.7	3614	8	AF113919	AF113919 Brassica
30	1106.2	39.4	1875	8	AF451980	AF451980 Papaver s
31	1093.4	38.9	1918	8	AF451979	AF451979 Papaver s
32	1092.6	38.9	3404	8	AF113918	AF113918 Brassica
33	1050	37.4	2397	8	AF451981	AF451981 Papaver s
34	1019.6	36.3	1886	8	AF428278	AF428278 Arabidops
35	891.8	31.8	148054	2	AC087553	AC087553 oryza sat
36	848.8	29.9	2067	8	AF451982	AF451982 Papaver s
37	758.6	27.0	148906	2	AB003629	AB003629 oryza sat
38	739.2	26.3	5169	8	AB001919	AB001919 oryza sat
39	624.6	22.2	4740	8	AF271357	AF271357 oryza sat
40	590.4	21.0	6672	8	AF271356	AF271356 oryza sat
41	585.6	20.9	148906	2	AP003629	AP003629 oryza sat
42	484.6	17.3	113663	2	AC099324	AC099324 oryza sat
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

2808 bp mRNA linear PLN 19-JUL-1996
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L33686
L33686.1 GI:1438074
phospholipase D.
Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids 1; Malpighiales; Euphorbiaceae; Ricinus.
1 (bases 1 to 2808)
Wang, X., Xu, L. and Zhong, L.
Cloning and expression of phosphatidylcholine hydrolyzing

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DB 2701 TGCAGGATTTGGGCTATCAGCAATGACAGATGTCATCTGCTGCTGCTGCTGCTGCT 2760
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RESULT 2
166478
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DEFINITION Sequence 1 from patent US 5670466.
ACCESSION 166478
VERSION 166478.1 GI:2724455
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2834)
AUTHORS Wang, X.
TITLE Recombinant DNA sequences encoding phospholipase
JOURNAL Patent: US 5670466-A 1 24-SEP-1997.
FEATURES
location/Qualifiers
source 1..2834
BASE COUNT 815 a 550 c 668 q 801 t
ORIGIN
Query Match 97.2% Score 2728.4; Db 6; Length 2844;
Best Local Similarity 99.1% Pred. No. 0;
Matches 2785; Conservative 0; Mismatches 21; Indels 4; Gaps 4;
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DB 129 CTCTCTCTGTTCT 188
QY 181 GCAGGAGACTCTACATGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 240
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DB 249 CCACCT 308
QY 301 TAGTAACT 360
DB 309 TAGTAACT 368
QY 361 GGAATTAACCAATTCAGGAGCT 420
DB 369 GGAATTAACCAATTCAGGAGCT 428

Db 460 TTCAATTTATTTGGCCATCTGGCTTCAATATTTATTTACTGTGAAAGATGATAATC 519
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QY 2397 CAGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2456
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QY 2517 AGTTTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2576
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RESULT 7
AF201661
LOCUS Lycopersicon esculentum phospholipase D alpha mRNA, partial cds.
DEFINITION
ACCESSION AF201661
VERSION AF201661.1 GI:6573118
KEYWORDS
SOURCE Lycopersicon esculentum.
ORGANISM Lycopersicon esculentum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE
1 (bases 1 to 2427)
Almqvist,K.C. and Paliyath,G.
Cloning and sequencing of a full-length cDNA coding for
phospholipase D alpha (Accession No. AF201661) from tomato (pGR
00-013)
Plant Physiol. 122 (1), 292 (2000)
2 (bases 1 to 2427)
Almqvist,K.C. and Paliyath,G.
Direct Submission
Submitted (03-NOV-1999) Food Science, University of Guelph, Gordon,
Guelph, ONT N1G 2W1, Canada
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Best Local Similarity 78.4%; Pred. No. 0;
Matches 1901; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
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DB 301 TTGGTGGCTATCTTAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 521 GAGATACATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
DB 361 GAGATG 420
QY 581 AAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 640
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QY 641 ATCAGAAAGTCAAAATATGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATG 700
DB 481 ATTAGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 701 AAGGTTTCTCTCTATCAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 760
DB 541 CAGGTTTCTCTCTATCAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600
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DB 601 TGTGGCGGAAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 821 AATGCAAAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 880
DB 661 AATGCAAAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
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ORIGIN

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Best Local Similarity 77.0%; Pred. No. 0;
Matches 1889; Conservative 0; Mismatches 560; Indels 4; Gaps 4;

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QY 203 ATCTATGAGTGGATTAAGCTTCACAGCGGAGGTGGTCCCCACTCTTTTGGTAAGCTTGTT 262
DB 161 ATCTTTGAGTTCATCACTTAA-AGCGGGGAGCGTGGTGGTATTTTGGGAAGCTTAAAG 219

QY 263 GAAATATTGAGGACAGACTTGCTTTTGGC-AAAGGAGTACTAATCACTATGCAACTAT 321
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 KEYWORDS
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 Brassica oleracea var. capitata.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 1 (bases 1 to 2743)
 Kim,D.U., Roh,T.Y., Lee,J., Noh,J.Y., Jang,Y.J., Hoo,K.L., Yoo,H.S.
 and Choi,M.O.
 Molecular cloning and functional expression of a phospholipase D
 from cabbage (Brassica oleracea var. capitata)
 Biochim. Biophys. Acta 1437 (3), 409-414 (1999)
 99203163
 10101274
 2 (bases 1 to 2743)
 Kim,D.U., Lee,J.E., Roh,T.Y., Choi,M.-U. and Yoo,H.S.
 Direct Submission
 Submitted (15-JAN-1997) Chemistry, Seoul National University,
 ShinKim-dong, Kwan-Ak-Gu, Seoul, Korea
 3 (bases 1 to 2743)
 Kim,D.U., Lee,J.E., Roh,T.Y., Choi,M.-U. and Yoo,H.S.
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 Sequence update by submitter
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ORGANISM     Brassica oleracea
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Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 2702)
Pannenberq, I., Mansfeld, J. and Ulbrich-Hofmann, R.
Identification of Two Isoenzymes (Accession Nos. AF090444 and
AF090445) of Phospholipase D from Cabbage (PGR98-188)
Plant Physiol. 118 (3), 1102 (1998)
2 (bases 1 to 2702)
Pannenberq, I., Mansfeld, J. and Ulbrich-Hofmann, R.
Direct Submission
Submitted (04-SEP-1998) Biochemistry/Biotechnology, M.-Luther
University, Kurt-Mothes-Strasse 3, Halle 06120, Germany
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RESULT 14
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LOCUS AF090445
DEFINITION Brassica oleracea phospholipase D1 (PLD1) mRNA, complete cds.
ACCESSION AF090445
VERSION AF090445.1 GI:4649088
KEYWORDS
SOURCE Brassica oleracea.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 2794)
AUTHORS Pannenberg, L., Mansfield, J. and Ulbrich-Hofmann, R.
TITLE Identification of Two Isoenzymes (Accession Nos. AF090444 and
AF090445) of Phospholipase D from Cabbage (PCR98-188)
JOURNAL Plant Physiol. 118 (3), 1102 (1998)
REFERENCE 2 (bases 1 to 2793)
AUTHORS Pannenberg, L., Mansfield, J. and Ulbrich-Hofmann, R.
TITLE Direct Submission
JOURNAL Submitted (04-Sep-1998) Biochemistry/Biotechnology, M.-Luther
University, Kurt-Mothes-Strasse 3, Halle 06120, Germany
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BASE COUNT 720 a 659 c 700 q 714 t
ORIGIN

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Best local Similarity 74.0%; pred. No. 0;
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AB017071
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AB017071.1 GI:3510447
Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui pl
clone:MSJ11.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1. (sites)
Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 3. I.
Sequence features of the regions of 4,504,864 bp covered by sixty
pl and YAC clones
DNA Res. 7 (2), 131-135 (2000)
2027480
2 (bases 1 to 81370)
Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S.
Direct Submission
Submitted (26-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research, 1542-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:yokakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/aad/graph.cgi?c=MSJ11
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/grail-1.4/),
GENSCAN (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://grcm1.zoology.stanford.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is M017 and the 3' clone is MW-8.
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Db 42622 TAACCGCATTTCTGACAAAGTATTGGGACTTTTACATCAAGTCACTGCAACATGACCT 42681

QY 2446 ACCTGGTCATTTCCTGCTATGCTATTGCGGTGCTAGTGAAGGAGATGTGACAGAGCT 2505
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QY 2506 CCGTGGAAATGAGCTTTTTCCTGACACGAGAGGCTGCTGTCTAGTGTGCHAAATTCATT 2565
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Search completed: May 5, 2003, 05:41:48
Job time : 8468.21 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2003, 22:29:11 : Search time 1313.07 Seconds
(without alignments)
9657.588 Million cell updates/sec

Title: US-09-817-869-1

Perfect score: 783

Sequence: 1 ttttccaaagacacagatg.....tcgtgacagatccatgggt 783

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3	489.6	62.5	512	10	AV525255	AV525255
4	446.6	57.0	538	9	A1994568	A1994568
5	444.2	56.7	765	17	BH436925	BH436925
6	426.4	54.5	812	10	BE052194	BE052194

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

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2 540 69.0 564 10 AV551602 AV551602

3 489.6 62.5 512 10 AV525255 AV525255

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3	489.6	62.5	512	10	AV525255	AV525255
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RESULT 2
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Rosidae; eustosids (1); Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 564)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)

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MEDLINE
COMMENT      20464094
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yata 1-4-2, Kizu, Kyoto, Japan 619-0422, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/eng/plant/.
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Db 181 CAGAGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 395 AGCTATATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454
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RESULT 4
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SOURCE     thale cress.

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 Db 244 AATTTATCTATATGAAATCATGATTTCTCGGAAGCTCATTTGACTGGAGTCTGTAT 303
 QY 243 GGTATTAATCTCTGAGGACATCAATGCCCTGCCTTAATCCAAAAGAGTTGCTGCTCAAG 302
 11
 Db 304 GAATTAAGCTCTAGGATTAATGCTTTGCATCTGATTCCTCAAGAACTTTTCATTAAA 363
 QY 303 ATAGTTAGCAAGATGATCAAGAGAGAGTTCAGGCTCTATGTTGTGTTTCAATGTGG 362
 11
 Db 364 ATTCTAGCAAGATGCAAGGAGGAGAGAGGTTTACCGTTTATGTTGTGCTCATGTGG 423
 QY 363 CCAGAAGTCTCCAGAGATGATCATGCTCAAGCTATATAGACTGGCAGAGAGACC 422
 11
 Db 424 CCAGAAGTATCCAGAGATGGCTCAGTTCAGTCAAGCTATATAGATTGGCAGAGAGACC 483
 QY 423 ATGAGATGATGTACAAGGATGTGATTCAGGCTCTCAAGGCTCTTGAGGGCCCGGAAGAT 482
 11
 Db 484 ATGACATGATGTATAGGATGTTATTCAGGCTCTCAAGCCAAAGGTTAGCGATGAGAA 543
 QY 483 CCAGAAGTATCTGACATCTCTTGTCTTGGAAACCGTGGAGTCAAGAAAGATGGAGAG 542
 11
 Db 544 CCAGAAGTATTTAATCATTTTCTGCTTGGGAACCGAGAGTTAAGAAGAGTGGAGAA 603
 QY 543 TATGAGTCTGCTGAGAAACAGACCCCGACACTGATATACATGAGGGGCGAAGAGCAGC 602
 11
 Db 604 TATGAACCGTCTGAAGACCCGACCTGATACAGATTTGCCAGAGCTCANGAGGCCGT 663
 QY 603 GCTTTCATGATTTACGTCCACACCAAAATGATGATGCTTCAGCATGAATCATTTATCAT 662
 11
 Db 664 GCTTTCATGATCTATGTTCTGCTAAATGATGATGCTGATGATGATGATGATGATGAT 723
 QY 663 GGTCTCTACATCAACCAAGAGTCAATGGAGGTCGAAGAGACTCTGAGATAGCAATG 722
 11
 Db 724 GGTCTCTCAACATCAACCAAGAGTCAATGGAGGTCGAAGAGACTCTGAGATAGCAATG 782
 QY 723 GAGGTTATCAAC 735
 11
 Db 783 GAGGCTTATCAAC 795

RESULT 7
 AV109642 2876 bp mRNA linear HTC 25-MAY-2002

DEFINITION Zea mays Cl1830_1 mRNA sequence.

ACCESSION AV109642

VERSION AV109642.1 GI:21213442

KEYWORDS HTC.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 2876)

Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S.,

Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

Maize Mapping Project/DuPont Consensus Sequences for Design of

Overgo Probes

Unpublished (2002)

2 (bases 1 to 2876)

Coe, E.C.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

LOCATION/Qualifiers

1..2876

/organism="Zea mays"

/db_xref="MaizeDB:630625"

/db_xref="taxon:4577"

/clone="Cl1830_1"

Library="Maize Mapping Project/DuPont Consensus

Library"

Note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of RACS in conjunction with the Maize Mapping Project"

BASE COUNT 636 a 709 c 779 g 623 t 129 others
 ORIGIN

Query Match

Best Local Similarity 54.8%; Score 425; DB 11; Length 2876;

Matches 562; Conservative 0; Mismatches 210; Indels 1; Gaps 1;

QY 11 GACACAGATGTGGGAATGCCAAATTTTGTAGTGTCAATGATGGAGAGTCTGCTGCG 70

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1484 GACAGAGAGACATGGAATGTCAGCTCTTCAGATCAAGATGCTGCTGCTGCTGCTG 1543

QY 71 TTCCCGAGTCCGCTCAAGCTCTGCGAAGGAGGCTTCTACAGTGGGAAATATAACAT 130

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1544 TTCCCGAGTCCGCTCAAGCTCTGCGAAGGAGGCTTCTACAGTGGGAAATATAACAT 1602

QY 131 CATTGATAGAGTATCCAAAGATGCTTACATTCATGCAATCAGACGCTGTAAAGATTTAT 190

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1603 CATTGATAGAGTATCCAAAGATGCTTACATTCATGCAATCAGACGCTGTAAAGATTTAT 1662

QY 191 CTACGTTGAAACAGTACTTCCTGCGAGTCTTTTGTGCGAGCGATGGTATTAC 250

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1663 CTACGTTGAAACAGTACTTCCTGCGAGTCTTTTGTGCGAGCGATGGTATTAC 1722

QY 251 TCTGAGGACATCAATTCGCTGACCTTAATCCCAAGAGCTTGTGCTCAAGATAGTAG 310

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1723 TCTGAGGACATCAATTCGCTGACCTTAATCCCAAGAGCTTGTGCTCAAGATAGTAG 1782

QY 311 CAAGATTGATCAAGAGAGAGAGTTCAGGCTCTAGTGTGCTGTAAATGCTGAGAG 370

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1783 CAAGATTGATCAAGAGAGAGTTCAGGCTCTAGTGTGCTGTAAATGCTGAGAG 1842

QY 371 TCTCCAGAGAGAGAGTTCAGGCTCTAGTGTGCTGTAAATGCTGAGAGAGAT 430

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1843 TCTCCAGAGAGAGAGTTCAGGCTCTAGTGTGCTGTAAATGCTGAGAGAGAT 1902

QY 431 GATGTACAGGATGCTGATTCAGGCTCTAGGCTCTAGGCTCTAGGCTCTAGGCTCTAG 490

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1903 GATGTACAGGATGCTGATTCAGGCTCTAGGCTCTAGGCTCTAGGCTCTAGGCTCTAG 1962

QY 491 CTATCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 1963 CTATCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2022

QY 551 TGTGAGAAACAGAGAGAGAGTTCAGGCTCTAGGCTCTAGGCTCTAGGCTCTAGGCTCTAG 610

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 2023 TGTGAGAAACAGAGAGAGTTCAGGCTCTAGGCTCTAGGCTCTAGGCTCTAGGCTCTAG 2082

QY 611 GATTTCCTCCACACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 670

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 2083 GATTTCCTCCACACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2142

QY 671 TAAATCAACACAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 730

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 2143 TAAATCAACACAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 2202

QY 731 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 783

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Db 2203 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 2255

QY 731 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 783

11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

Db 2203 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 2255

QY 731 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 783

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Db 2203 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 2255

QY 731 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 783

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Db 2203 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 2255

QY 731 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 783

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Db 2203 TCAAGACATCACTTGTGCTGATGAGAGTCTGATGAGAGTCTGATGAGAGTCTGATGAGAG 2255

RESULT 8

AV550884

LOCUS

AV550884

548 bp

mRNA

linear

EST 06-SEP-2000

QY 234 GCACCCGATGTAATACCTCTGAGGACATCAATGGCCCTGCACCTTAATCCAAAGAGTTG 293
 Db 136 AGTGGCTGATGATTAAGCGCTGAAGACATTTGGCTTTGCATCTAATCCCAAGAACTT 195
 QY 294 TCGTCGAATAGTTACCAAGATTGATCAGGAGAGAAATTCAGGGCTCTATGTTGCGTT 353
 Db 196 TCACCTCAAGATTGTTAGTAAGATTGAAGCTGGGAAAGGTTTCTGCTGTAATGTTAGTTC 255
 QY 354 CCAATGTGSCCAGAAAGTCTCCGAGAGAGTGGATCAGTCCAAAGCTATATAGACTGGCAG 413
 Db 256 CCAATGTGSCCAGAGAGTCTCCGAGAAAGTGGATCAGTCCAAAGCTATATAGACTGGCAG 315
 QY 414 AAGAGACCAATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 473
 Db 316 AAGAGACCAATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 375
 QY 474 CCGAAGATCCAGAAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 533
 Db 376 GATGAGATGCTGAAACTATTTGACATTTCTGCTTGGCAACCGGGAAGTGAAGAA 435
 QY 534 GATGGAGATGATGAGTGTGTTGAGAAACACGACCGGACACTGATTACATGAGGGCGCAA 593
 Db 436 CCAGGAGAAATGATGAGCTTCTGAGCAACAGATCCTGATTCAGATTATCAGAGAGCCAA 495
 QY 594 GAACAGCGCGTTTCATGATTTACGTCACACACCAAAATGATGATGATGATGATGATGATGATG 653
 Db 496 GAGCGCGGAGGATTCATGATTTAATGTTATACCAAGATGATGATGATGATGATGATGATGATG 555
 QY 654 ATTATCATGGTCTGCTACATCAACGAGAGTCAATGACGCGTGCAGAGACTCTGAG 713
 Db 556 ATAATGTTGGATGCTGCAATATCAACCAAAATGATGATGATGATGATGATGATGATGATGATG 615
 QY 714 ATAGCAATGGAGGT 728
 Db 616 ATTCCATGGGTGCT 630

RESULT 10
 BQ148267
 LOCUS BQ148267 656 bp mRNA linear EST 24-APR-2002
 DEFINITION NF065C03FLF1022 developing flower Medicago truncatula cDNA clone
 NF065C03FLF 5', mRNA sequence.

ACCESSION BQ148267
 VERSION BQ148267.1 GI:20285326

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 656)
 Torres-Jerez, L., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
 Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula flower library

JOURNAL Unpublished (2001)
 COMMENT Contact: May GD

Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391

Fax: 580 221 7380
 Email: qdmay@noble.org

Insert Length: 656 Std Error: 0.00
 Plate: 065 row: C column: 03
 Seq primer: TCACACAGGAACACGATCAC.

location/Qualifiers
 1..656

/organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF065C03FL"
 /clone_lib="Developing flower"

FEATURES
 source

/tissue_type="developing flowers"
 /dev_stage="developmentally pooled. Contains a mixture of
 very young, developing, fully-opened flowers and flowers
 in early transition into pods."
 /note="Vector: Lambda Zap; cDNA was prepared from polyA-
 enriched, pooled samples of equivalent amounts of total
 RNA from very young, developing, fully-opened flowers and
 flowers transitioning into pods. The cDNA was
 directionally ligated into the Uni-Zap XR vector
 (Stratagene) and packaged using the GigaPack III gold
 packaging extracts. Phagemids containing cDNA inserts were
 in vivo excised from the recombinant Uni-Zap XR vector
 using EXASist helper phage and the E. coli strain
 XL1-blue MRF' (Stratagene). Excised plasmids were plated
 using SOLR cells."

BASE COUNT 193 a 111 c 167 g 184 t 1 others

Query Match 48.1%; Score 376.8; DB 14; Length 656;
 Best Local Similarity 74.7%; Pred. No. 9,26,100;
 Matches 485; Conservative 0; Mismatches 163; Indels 1; Gaps 1;

QY 11 GACCAAGATGTGTGAATGTCGAATGTTTAGTCTCATGATGAGAGACTGCTGTCTGG 70
 Db 11 GACCAAGATGTGTGAATGTCGAATGTTTAGTCTCATGATGAGAGACTGCTGTCTGG 70
 QY 5 GATCAAGAGACGTTGAATGTTTCAAGCTATTTAGATGATGAGAGAGAGAGAGAGAGAG 64
 Db 5 GATCAAGAGACGTTGAATGTTTCAAGCTATTTAGATGATGAGAGAGAGAGAGAGAGAG 64
 QY 71 TTTCGAGTGGCTGAGGCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 130
 Db 71 TTTCGAGTGGCTGAGGCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 130
 QY 65 TTCCCGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 124
 Db 65 TTCCCGAGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 124
 QY 131 CATTCATAGAGATGATCAAGATGCTTACATTCATGATGATGATGATGATGATGATGATGAT 190
 Db 131 CATTCATAGAGATGATCAAGATGCTTACATTCATGATGATGATGATGATGATGATGATGAT 190
 QY 125 AATAGATAGAGATGATTCAGATGCTTATATCAATGATGATGATGATGATGATGATGATGAT 184
 Db 125 AATAGATAGAGATGATTCAGATGCTTATATCAATGATGATGATGATGATGATGATGATGAT 184
 QY 191 CTACGTTGAAACCGAGTACTTCTTGGAGAGTCTTTTGGTGGAGAGAGAGAGAGAGAGAG 250
 Db 191 CTACGTTGAAACCGAGTACTTCTTGGAGAGTCTTTTGGTGGAGAGAGAGAGAGAGAGAG 250
 QY 185 CTACATGAAATCAATATTTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAG 244
 Db 185 CTACATGAAATCAATATTTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAG 244
 QY 251 TCTGAGGAGATCAATGCTGCTGACCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 310
 Db 251 TCTGAGGAGATCAATGCTGCTGACCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 310
 QY 245 GCTGAGAGATGTTGGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGG 304
 Db 245 GCTGAGAGATGTTGGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGGAGAGTCTTGG 304
 QY 311 CAAGATTTGATCAAG 370
 Db 311 CAAGATTTGATCAAG 370
 QY 305 CAAGATTTGAGAGTGGGAG 364
 Db 305 CAAGATTTGAGAGTGGGAG 364
 QY 371 TCTCCAGAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 430
 Db 371 TCTCCAGAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 430
 QY 365 TGTCGAGAGAGTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
 Db 365 TGTCGAGAGAGTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
 QY 431 GATGTATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
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 QY 425 GATGTATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 484
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 QY 491 CATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
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 QY 485 CATTTTGACATGCTTCTGCTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
 Db 485 CATTTTGACATGCTTCTGCTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
 QY 551 TCGTGAAG 610
 Db 551 TCGTGAAG 610
 QY 545 TCGTGAAG 604
 Db 545 TCGTGAAG 604
 QY 611 GATTTCAGTCTCAACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
 Db 611 GATTTCAGTCTCAACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
 QY 605 GATCTATGTTTCCCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654
 Db 605 GATCTATGTTTCCCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654

RESULT 11
 BQ131122

LOCUS BQ131122

DEFINITION

BQ131122 806 bp mRNA linear EST 20-FEB-2001
 L48 1074F4 ice plant Lambda Uni-Zap XR expression library; 48 hours
 NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1074
 5', mRNA sequence.

directionally cloned into the EcoRI-XhoI restriction site of the phuscript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the Laboratory of Dr. Randy Shoemaker."

```

BASE COUNT      178 a   104 c   143 g   162 t
ORIGIN

Query Match      46.0%; Score 360; DB 13; Length 587;
Best Local Similarity 76.9%; Pred. No. 7.6e-95;
Matches 452; Conservative 0; Mismatches 135; Indels 1; Gaps 1;

QY 75 CCAGAGCTGCTGAGCTGCTGCGAAGCCGCGCTTCAGAGTGGGAAAGATAACATCAT 134
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Db 1 CGAGAGCTGCTGAGAGTCTCCAGAGCTGGTCTTAT-TAGTGGGAGGATAATATCAT 59

QY 135 GATGAGAGTACCAAGATGTTACATTCATGCAACAGAGCTGCTAAGGATTCATCTAC 194
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Db 60 GATCGTAGCAATTCAGATGCTTATATTAATGCTATTGCGAGCTGCAAGAACATTCATCTAT 119

QY 195 GTTCAAAACAGTACTTCTTGGGAGTCTCTTTTCTTGGGAGCCGATGCTATTACTCTCT 254
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Db 120 ATTGAAGATCAGTATTTCTTGGAGGCTCTTTTGGCTGGAGTCTGATGATATTAGGCTT 179

QY 255 GAGGACATCAAGCCCTGCACTTAATCCCAAGAGCTGTGCGTGAAGATAGTAGCAAG 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 GAAGACATTTGCTGCTTTGCACTAATCCCAAGAGAACTTTCACCTCAAGATTTGTTAGTAG 239

QY 315 ATTGATCAAGAGAGAGTTCAGGCTCTATGTTGTGTTCCCAATGTGGCCAGAGGCTTC 374
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 ATTGAAGCTGGGAAAGGTTTGTGTTGATGTTGTGTTAGTCCCAATGTGGCCAGAGGTTGT 299

QY 375 CCAGAGATGCTGATGCTGCAAGCTATATATTAGCTGGCAGAGGAGGACCATGGAGATGATG 434
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 CCAGAGATGCTGATGCTGCAAGCTATATATTAGCTGGCAGAGGAGGACCATGGAGATGATG 359

QY 435 TACAAGATGATGATGATGCTGCAAGGCTTCAGAGGCTTCAGAGGCGGCAAGATCCAGAAACTAT 494
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 TACAAGACATTTATCAGGACCTCAGAGCTTAAGGGAATGATGAAGATGCTCGAAACTAT 419

QY 495 CTGACATCTCTGCTTGGAAACGGTGGAGTCAAGAAAGATGAGAGATGATGAGCTGCT 554
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 420 TTGACATCTCTGCTTGGCAACGGGAAGTGAAGAAACCCAGAGAAATGAGCCTCT 479

QY 555 GAGAAACAGACCCGACACTATATACATGAGGCGCCAGAAAGCAGCGCTTTTCATGATT 614
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 GAGCAACCAAGTCTGATTCAGATTTATCAGAGAGCCCAAGAGGCCCGCAGCATTCATGATT 539

QY 615 TAGCTCCACACCAAAATGATGCTGTTGAGGATGAATACATTTATCATTT 662
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 540 TATGTTATACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587

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RESULT 13

HC594748 699 bp mRNA linear EST 12-APR-2001
 EST492426 cSTS Solanum tuberosum cDNA clone cSTS56 5' sequence,
 mRNA sequence.

HC594748

HC594748.1 GI:13611888

EST.

Solanum tuberosum

potato.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 699)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chieming, A.,

Bouqri, O., Buell, C.R., Renning, C., Tanksley, S. and Baker, B.

Generations of ESTs from sprouting potato eyes

Unpublished (2000)

Contact: Cathy Renning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email edna@resgen.com
 Seq primer: M13F-R.

FEATURES

Source

1..699
 /organism="Solanum tuberosum"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cSTS56"
 /clone_lib="cSTS"
 /issue_type="Sprouting eyes from tubers"
 /dev_stage="12-14 weeks post harvest"
 /lab_host="SOLR"

/note="vector: phuscript SK(-); Site_1: EcoRI; Site_2:
 XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
 taken from tubers. The tubers were incubated at 26C in the
 dark for 2-3 weeks prior to sprouting. The eyes were
 frozen in liquid nitrogen immediately upon removal from
 tubers."

BASE COUNT 211 a 115 c 181 g 192 t

ORIGIN

Query Match 45.8%; Score 459; DB 12; Length 699;

Best Local Similarity 73.7%; Pred. No. 1.7e-97;

Matches 483; Conservative 0; Mismatches 170; Indels 2; Gaps 2;

QY 11 GACCACGATGCTGGAATGTCACATTTGTTAGTTCATGATGAGAGAGCTGCTGCTGG 70

Db 40 GATCATGAACATGAAATGTTTCAGTTATTCATCAATGATGAGAGAGCTGCTGCTGG 99

QY 71 TTTCCCGAGTCCGCTGAAGCTGCTGCGGAAAGGCGCTGTGTATGATGAGAGAGATAACAT 130

Db 100 TTCTCTGACACCTGAGAGATGACGACAAAGAGTGGCTTGT CAGTGGCAAGATAACAT 158

QY 131 CATTCATAGAGATATCAAGATGCTTATTCATGCAATCAACAGCTGCTAAGATATTCAT 190

Db 159 AATTGATAGAGATATCAAGATGCTTATTCATGCAATCAACAGCTGCTAAGATATTCAT 218

QY 191 CTACGTTGAAACACGATATTCGTTGGAGTCTCTTGTGTCGAGAGAGTATTATG 250

Db 219 TTACATTTGAAATCAGTATTTCTTGGAACTGTGCACTAGATGAGATATTCAT 278

QY 251 TCTGAGGACATCAATGCTCTGACTTAATCCGAAAGAGTGTGTGTGAAATATCTAG 310

Db 279 GGTAGAGAGCTGAGGTGCTTTCATGTCATTCGAAAGAACTTGCATTCGAGATTGTCAG 338

QY 311 CAAGATTGATCAAGAGAGAGAGCTTCAGGCTCTATCTTGGTTCGAGAGTGTGAGAG 370

Db 339 TAAGATTGAGCCGCGGAAAGGTTTACGTTTATGTTGGTTCGAGAGTGTGAGAGAG 398

QY 371 TCTCCAGAGAGTGGATCAGTGCAGCTATATTAGACTGGCAGAGAGAGATCATGATAT 430

Db 399 AATCCCGAAGGTGATCATGACAGGCAATATTAGACTGGCAGAGAGAGATCATGATAT 458

QY 431 GATGTACAGAGATGATTCAGGCTCTCAAGGCTCTTGAAGGCTCTTGAAGGCTCTTGAAG 490

Db 459 GATGATTAAGTACATTTTCAGAGCAATGATGCTTAAAGTATTCGAGAGAGATTCAGAG 518

QY 491 CTATCTGACATCTCTGCTGCTTGAAGGCTCTTGAAGGCTCTTGAAGGCTCTTGAAGG 550

Db 519 TTATTTGACATTTTCTGCTGCTTGAAGGCTCTTGAAGGCTCTTGAAGGCTCTTGAAGG 578

QY 551 TGTGAGAAACAG 610

Db 579 TTTGAG 637

QY 611 GATTACGTCACATCAAAATGATGATGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 665

Db 638 GATATATGTCATTCAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 692

RESULT 14

234674


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Db 422 TGAATGCAAAAGGAGGACGATGAGATGATATAAAGATATTATTCAAGCTTTACAAAA 381
QY 464 TCTTGAGGCGCCGCAAGATCCAGAACTATCTGACATCTCTGCTCTGGAAACGGTGA 523
Db 382 CAAAGGGCTTGAGAGGAGCCCTAGAGATTACCTACATCTTTTGGCTTGGGAATCGTGA 441
QY 524 GGTCAAGAAAGATGAGAGTATGAGCTGCTGAGAAACGAGACCGCGACACTGATTACAT 583
Db 442 AATGAAAAAGGATGGTGTGATGATCAACCTTCGGAGGCTCCGAGCCCGGAATCAAAATTACCA 501
QY 584 GAGGGCGCAAGAGACGCGCTTTCATGATTTACGTCCACACCAAAATGATCGTTGA 643
Db 502 TAAAGCCCAACAACGCGCGGCTTTATGATCTACGTCCATGCGCAAAATGATGATAGTTGA 561
QY 644 CGATGAATACATATGATGCTGCTTAACATCAACAGAGGTCAATGACGGTGCAG 703
Db 562 TGACGAATATATAATAGTGGATCTCGGACATTAATCAACGATCAATGGATGGGCAG 621
QY 704 AACCTCTGAGATAGCAATGGAGGTTATCAAGCACAATCCTTGTCCATAGACACCCAGC 763
Db 622 GGATTCGAAATAGCAATGGAGCTTACCAACCTCATCACTTGTCTACACGGCACACCCGC 681
QY 764 TCGTGGCCAGATCCATGGGT 783
Db 682 AAGGGATGAAGTTCATGGTT 701

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Job time : 1321.07 secs

GenCore version 5.1.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2003, 22:40:50 : Search time 98.1203 Seconds

(without alignments)
9429.336 Million cell updates/sec

Title: US-09-817-869-1

Perfect score: 783

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	783	100.0	783	9	US-09-817-869-1
2	535.6	68.4	1062	10	US-09-770-445-144
3	489.6	62.5	2808	9	US-09-817-869-2
4	482.6	61.6	2736	9	US-10-078-770-123
5	428.2	54.7	2957	9	US-10-078-770-125
6	197	25.2	2571	9	US-09-938-842A-487
7	173	22.1	2797	9	US-10-078-770-133
8	166.4	21.3	271	10	US-09-878-574-911
9	136.4	17.4	261	10	US-09-878-574-9127
10	128.4	16.4	202	10	US-09-878-574-8447
11	103.6	13.2	833	10	US-09-770-445-688
12	97.8	12.5	452	10	US-09-770-444-643
13	83.4	10.7	866	9	US-10-078-770-131
14	82.2	10.5	387	9	US-10-078-770-127
15	76.2	9.7	182	10	US-09-878-574-6135
16	47.8	6.1	1070	10	US-09-770-445-134
17	41.8	5.3	419	10	US-09-960-352-6040
18	41	5.2	434	10	US-09-960-352-7449
19	37.6	4.8	5727	9	US-09-896-594-18

C	20	37.6	4.8	6757	9	US-09-896-594-18	Sequence 16, Appl
	21	37.6	4.8	7236	9	US-09-896-594-19	Sequence 19, Appl
	22	37.6	4.8	8272	9	US-09-896-594-17	Sequence 17, Appl
	23	37.2	4.8	671	9	US-10-184-644-346	Sequence 346, App
	24	37.2	4.8	671	9	US-10-184-644-346	Sequence 346, App
	25	36.2	4.6	7256	9	US-09-896-594-23	Sequence 23, Appl
	26	36.2	4.6	7639	9	US-09-896-594-21	Sequence 21, Appl
C	27	34.8	4.4	515	9	US-10-184-644-76	Sequence 76, Appl
	28	34.8	4.4	515	9	US-10-184-644-76	Sequence 76, Appl
	29	33.8	4.3	2226	10	US-09-815-242-4934	Sequence 3944, Ap
	30	33.8	4.3	2229	10	US-09-815-242-6537	Sequence 6547, Ap
C	31	33.4	4.3	1359	9	US-09-764-891-2309	Sequence 2309, Ap
	32	32.8	4.2	1184	9	US-10-123-155-412	Sequence 412, App
	33	32.2	4.1	345	10	US-09-770-791-771	Sequence 771, App
	34	32.2	4.1	1070	10	US-09-770-445-135	Sequence 135, App
	35	32	4.1	1024	9	US-10-124-155-198	Sequence 198, App
	36	32	4.1	1824	10	US-09-815-242-9693	Sequence 9693, Ap
	37	32	4.1	14955	10	US-09-961-527A-1	Sequence 1, Appl
C	38	31.8	4.1	760	10	US-09-864-864-13	Sequence 13, Appl
	39	31.4	4.0	834	10	US-09-887-576-808	Sequence 808, App
C	40	31.4	4.0	1744	10	US-09-804-682-78	Sequence 78, Appl
	41	31.2	4.0	811	9	US-10-184-644-414	Sequence 414, App
	42	31.2	4.0	811	9	US-10-184-644-414	Sequence 414, App
	43	31	4.0	390	10	US-09-864-761-12004	Sequence 28584, A
	44	31	4.0	582	10	US-09-864-761-12004	Sequence 12004, A
C	45	31	4.0	792	10	US-09-895-828-458	Sequence 458, App

ALIGNMENTS

RESULT 1
US-09-817-869-1
: Sequence 1, Application US/09817869
: Publication No. US20030074692A1
: GENERAL INFORMATION:
: APPLICANT: WANG, XUEMIN
: APPLICANT: YONGMING, SANG
: TITLE OF INVENTION: DROUGHT TOLERANT PLANTS AND METHODS OF INCREASING DROUGHT TOL
: TITLE OF INVENTION: PLANTS
: FILE REFERENCE: 30509
: CURRENT APPLICATION NUMBER: US/09/817,869
: CURRENT FILING DATE: 2002-07-11
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 783
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-817-869-1

Query Match	100.0%	Score 783	DB 9	Length 783
Best Local Similarity	100.0%	Pred. No. 2.4e-257		
Matches 783:	Conservative	0	Mismatches	0
		0	Indels	0
		0	Gaps	0
QY	1	TGTTCCAGAGACACGATGTGTGGAAATGTCGAATTTAGTTCATTGAGGAGAGC	60	
DB	1	TGTTCCAGAGACACGATGTGTGGAAATGTCGAATTTAGTTCATTGAGGAGAGC	60	
QY	61	TGCTGTGGATTTCCGAGTTCGGCTGAATCTGTGAGAGAGTGGGCTGTGTAATGGGA	120	
DB	61	TGCTGTGGATTTCCGAGTTCGGCTGAATCTGTGAGAGAGTGGGCTGTGTAATGGGA	120	
QY	121	AAGATAACATCATGATAGAGATATCCAGATCTTATCATTCATCAATCAGACATGCTTA	180	
DB	121	AAGATAACATCATGATAGAGATATCCAGATCTTATCATTCATCAATCAGACATGCTTA	180	
QY	181	AGGATTTCATCATGATGAGAAACAGATCTTCTGTGGAGTCTTTTGTGTGGAGAGCG	240	
DB	181	AGGATTTCATCATGATGAGAAACAGATCTTCTGTGGAGTCTTTTGTGTGGAGAGCG	240	
QY	241	ATGGTATTACTCTGAGGACATCAATGGCTGCACCTTAATCCAAAGAGTTGTCTCTGA	300	


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QY 4  TTTAAGAGACACGATGCTGGAAATGTCCAAATGTTTAGTCCATGATGAGGAGCTGC 63
DB 1522  TCTATGACACTTGTAGGACATGAAATGCTCCAGTGTGTTAGATCCATGATGTTGGAGCTGC 1581
QY 64  TCTGAGGTTTCCGAGTGCCTGAGAGCTGCTGCGGAACCGGCTTTACAGTGGGAAG 123
DB 1582  ATTGCTTCCGTTGAGACACCTGAGATGCGCCAGAGGCTGAGCTGTGTT-CAGTGGAAAGG 1640
QY 124  ATAACATCATGATAGAGATATCCAGATGCTTACATTCATCAATCAACAGCTGCTAAGG 183
DB 1641  ATAACATCATGACCAAGATTTACAGATGCTTATATCATCCATTCGAAGGGCAAGA 1700
QY 184  ATTTCATGAGTTGAAAACAGTACTTCCCTTGGGAGTTCTTTTCTGTTGGGAGCGGATG 243
DB 1701  ATTTTATTATATGAAATACAGTATTTCCCTTGGAGTCTTTTGGTGGAGCTGCTGATG 1760
QY 244  GTATTACTCTGAGACATCAATGCCCTGCACTTATCCCAAGAGTGTGCTGCAAGA 303
DB 1761  GTATTAGGCTGAGGATATTAATGCACTGCATCTAATACCAAGGAACTTTCACTCAAGA 1820
QY 304  TAGTTAGCAAGATTGATCAAGAGAGAGAGTTCAGGCTCTATGTTGTTGCTCAATGCTGC 363
DB 1821  TACTTAGCAAGATTGGGCAAGGAGAGAGTTCACGTGTTACATGTTGTTCCATGCTGC 1880
QY 364  CAGAAGGCTCCGAGAGAGTGGATCAGTGCAAGCTATATTAGACTGGCAGAGGAGCAACA 423
DB 1881  CAGAAGGCTATCCAGAGAGTGGATCAGTTCAAGCTATATTAGATTGGCAGAGAGGACAA 1940
QY 424  TCGAGATGATGATCAAGAGATGATGATCAGGCTCTCAAGGCTCTTCAAGGCCCGGAGATC 483
DB 1941  TCGAAATGATGATTAAGAGATATGTGCAAGCTCTCAAGGCTCTCAAGGCTCTTATGAGGATC 2000
QY 484  CAAGAATATCTGACATCTCTGCTGCTGGAACCGTGAGTCAAGTCAAGAGATGGAGACT 543
DB 2001  CTGGAACATATCTGACATCTCTGCTGCTGGAACCGTGAGTCAAGTCAAGAGATGGAGAT 2060
QY 544  ATGAGCTGCTGAGAAACCAAGAGAGAGTCAATGATGAGGCGGCAAGAGAGAGAGAGTGC 603
DB 2061  ATCAACCTGCAAGAAACCAAGAGAGTCAATGATGAGGCGGCAAGAGAGAGAGAGTGC 2120
QY 604  GTTTCATGATTTAGTCCAGACCAAAATGATATCGTTGACGATGATGATGATGATGATG 663
DB 2121  GTTTCATGATTTAGTCCAGACCAAAATGATATCGGATGATGATGATGATGATGATGATG 2180
QY 664  GGTCTGCTTAACATCAACAGAGTCAATGAGGCTGCAAGAGACTCTGAGATGAGCAATG 723
DB 2181  GATCTGCAACATCAACAGAGATCAATGATGATGATGATGATGATGATGATGATGATGATG 2240
QY 724  GAGGTATCAACACATCACTTGTGCTATAGACAAACAGCTGCTGCTGCTGCTGCTGCTGCT 783
DB 2241  GAGGCTATCAACACATCACTTGTGCTATAGACAAACAGCTGCTGCTGCTGCTGCTGCTGCT 2300

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RESULT 4
US-10-078-770-123
: Sequence 123, Application US/10078770
: Publication No. US2003003471A1
: GENERAL INFORMATION:
: APPLICANT: Farnold, Omolayo O.
: APPLICANT: Forde, Charlie
: APPLICANT: Miao, Guo-Hua
: TITLE OF INVENTION: cDNAs Encoding Polypeptides
: FILE REFERENCE: BH-1365 US NA
: CURRENT APPLICATION NUMBER: US/10/078,770
: CURRENT FILING DATE: 2002-02-19
: PRIOR APPLICATION NUMBER: 09/614,188
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: 60/143,400
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/153,534
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: 60/161,223

```

```

: PRIOR FILING DATE: 1999-10-22
: PRIOR APPLICATION NUMBER: 60/159,878
: PRIOR FILING DATE: 1999-10-15
: PRIOR APPLICATION NUMBER: 60/157,401
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/143,419
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/143,409
: PRIOR FILING DATE: 1999-07-12
: NUMBER OF SEQ ID NOS: 196
: SOFTWARE: Microsoft Office 97
: SEQ ID NO: 123
: LENGTH: 2736
: TYPE: DNA
: ORGANISM: Glycine max
US-10-078-770-123

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Query Match 61.6%; Score 482.6; DB 9; Length 2736;
Best Local Similarity 77.0%; Pred. No. 3,90-154;
Matches 601; Conservative 0; Mismatches 179; Indels 1; Gaps 1;
QY 3  TTCCAAGAGACACCATGTTGGAAATGCCAAATGTTTAGTCCATGATGAGGAGCTGC 62
DB 1477  TTCTGAGATCATGAGACCTGGAAATGTTCAATGTTTAGATCCATGATGTTGGAGCTGC 1546
QY 63  CTGCTGGGTTTCCGAGTGCCTGAAAGCTGTTGGGAAGCGGAGCTGTTACAGTGGGAAA 122
DB 1537  CTTTGGGTTCCCGAGACTCTGGAAGATGTTGGCAGAGTGGTCTTAT-TAGTGGGAAG 1545
QY 123  CATAACATCATGATAGAGATGATCAAGATGCTTACATTCATGATGATGATGATGATG 182
DB 1596  GATAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1655
QY 183  GATTCATCTAGTGTGGAAGACAGTACTGCTTGGAGTCTTGGAGTCTTGGAGTCTTGGAG 242
DB 1656  AACTTCATCTATTTGAAATCAGTATTTCTTGGAGTCTTGGAGTCTTGGAGTCTTGGAG 1715
QY 243  GGTATTACTCTGAGGATATCAATGCTGCTGCTTAAATGCTGCTGCTGCTGCTGCTGCTG 302
DB 1716  GATATTAAAGCTGAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1775
QY 303  ATAGTTAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 362
DB 1776  ATTTAGTAAAGTGAAGCTGAGGAAAGGTTTGTGCTGATGTTGCTGATGATGATGATG 1835
QY 363  CCAGAGCTCTCCAGAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
DB 1836  CCAGAGAGTGTTCAGAAAGTGCATGATGATGATGATGATGATGATGATGATGATGATG 1895
QY 423  ATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
DB 1896  ATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1955
QY 483  CCAGAAACTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 542
DB 1956  CCTCGAAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2015
QY 543  TATGAGCTGTGTGAGAAACCAAGACCTGATGATGATGATGATGATGATGATGATGATG 602
DB 2016  TATGAGCTGTGTGAGAAACCAAGACCTGATGATGATGATGATGATGATGATGATGATG 2075
QY 603  GCTTTCATGATTTAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662
DB 2076  CCATTCATGATTTAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2135
QY 663  GGGTCTGCTAATCAATCAAGAGAGTATGATGATGATGATGATGATGATGATGATGATG 722
DB 2136  GGATCTGCTAATCAATCAAGAGAGTATGATGATGATGATGATGATGATGATGATGATG 2195
QY 723  GGAGGTATCAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 782
DB 2196  GGAGGTATCAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2255

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1671 TTACATTCAGAACCAATATTTCTTGATCTTCATTCAGCTGGG-----ATTC 1718
251 TCTTGAGCATCAATACGCTGCATTAATCCCAAAAGAGTTGCTGCTCAAGATAGTAG 310
1719 AAACAAGAGCTGGTCTTAATAATCTAATCCCGATGGAAATCGGCTTANGATTCCTAA 1778
311 CAAGATTATCAAGAGAGAGAGTTCAGGCTCTATGTTGGTGTCCAAATGTGGCCAGAAG 370
1779 TAAGATTAGACGAGGAGGAATTTCTGCTGTTATTTGTTCAATCCCAATGTGGCCAGAAG 1838
371 TCTCCGAGAGTGGATCAGTCAAGCTATATTAGACTGTCAGAGGAGGAGGACCATGAGAT 430
1839 TGCTCCCAAGAAGTAAGCTATTCAAGATTTCTTACTGGCAGCACAACACCATGCAAT 1898
431 GATGTACAAGCATGTGATTGAGCTCTCAAG-----GCTCTTGGAGGCGCCGAAGATCC 484
1899 GATGTATCAACCATCTACAAAGCCACTCTGGAAGTTGGTCTTGATGGCCAGCTTGAGCC 1958
485 AAGAACTATCTGACATTTCTGCTTGGAAACCGTGAGGTCAAGAAAG-----534
1959 ACAAGACTTTTGAACCTTTCTCTCTTGGAAACAGAGAGGTTGGAACCAAGAGAGCTTC 2018
535 -----ATGGAGATATGAGCTGCTCAAG-----ATGAGAGATATGAGCTGCTGAGAAACCAACACCCGACACTGATTA 580
2019 TGATGAAACATTAATGATATATTTGCTCGGAGGCCACTCGAGCCAAATGCTGCACA 2078
581 CATGAGGCGCAAGACGCGCTTTCATGATTTAGTCCACACCAACCAAAATGATGCTG 640
2079 GGTGCAAGCTTTGAAGCTGAGATTCATGATATATGTTTCATTCCAAGGATGTTAGT 2138
641 IGAGGATGAATATTAATATCATGCTGCTGCTAGCATCAACAGAGGTCAATGAGCGTGC 700
2139 GGATGATGAGTTGCTTAATTTGCTTCCGCGGAATATCAACCAAGAGATCCCTGCAAGGAA 2198
701 AAGAGACTCTGAGATACCAATGAGGTTTATCAACCAACATCACTGTTGCCAIPAGACAAC 760
2199 TAGAGCACTGAATCGTATCGGAGGATATCAGCCACATCATTCATTCATGAGGCTAAGAAAG 2258
761 AGCTGCT 767
2259 TTCTGCT 2265

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US-10-078-770-133
: Sequence 133, Application US/10078770
: Publication No. US20030003471A1
: GENERAL INFORMATION:
: APPLICANT: Famodu, Omolayo O.
: APPLICANT: Miao, Guo-Hua
: TITLE OF INVENTION: cDNAs Encoding Polypeptides
: FILE REFERENCE: HR-1365 US NA
: CURRENT APPLICATION NUMBER: US/10/078,770
: CURRENT FILING DATE: 2002-02-19
: PRIOR APPLICATION NUMBER: 09/614,188
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: 60/143,400
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/153,534
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: 60/161,223
: PRIOR FILING DATE: 1999-10-22
: PRIOR APPLICATION NUMBER: 60/159,878
: PRIOR FILING DATE: 1999-10-15
: PRIOR APPLICATION NUMBER: 60/157,401
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/143,419
: PRIOR FILING DATE: 1999-07-12
: PRIOR APPLICATION NUMBER: 60/143,409
: PRIOR FILING DATE: 1999-07-12
: NUMBER OF SEQ ID NOS: 196

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: SOFTWARE: Microsoft Office 97
: SEQ ID NO 133
: LENGTH: 2797
: TYPE: DNA
: ORGANISM: Glycine max
US-10-078-770-133

Query Match      22.1%   Score 173;   DB 9;   Length 2797;
Best Local Similarity 56.1%   Pred. No. 4,10-48;
Matches 418;   Conservative 0;   Mismatches 305;   Indels 22;   Gaps 4;

QY 7 AAGAGACACGATGTTGGAAATGTCCAAATGTTTAAAGTTCATTCATGATGAGTCTGCTGC 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1463 AAATAACCGGAGACTTTGGCATCGCGAGTCTTGGCTTCAATGATTCATTCCTGTA 1522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 TGGGTTTCGCGAGTCCGCTCAAGCTGCTCGGGAAGTGGGGTTGTACAGTGGAAAGATA 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1523 AGGATTTCGAAGACCAACAAAGTCT-ATAAGAGAGCAACTTGGTTTCTGGAAAGAG 1581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 ACATCATTCATAGAGATATCCAAAGATGTTTAATATCATCAATCAATATGCTTAAGAT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1582 TACTGATACATGAGCATATCAGCTATGTCAGGCAATTCGCAAGCAATTCGCAAGCA 1641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 187 TCATCTACGTTGAAAACCACTACTTCTCTGGAGTCTTTTCTGTTGAGGCAAGTATA 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1642 TTATCTATATTGAGAACCAATACTTTCTTGGCTGCTCATATAAATGGG 1689
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 247 TTATCTCAGGACATCAATGCCCTGCTAAATTCGCAAAAGAGTTGTCGCTCAAGATAG 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1690 ATTCTTACAAAGACCTTGGTGCAGCAACTTAATTCGAAAGCAATTCATTAAGAAATAG 1749
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 307 TTAGCAAGATTCATCAAGAGAGAGAGTTTCAGAGTCTATGTTGTTGTTGCAATGTTAG 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1750 CCAATAAAATCAAAACATGACAGATTTCTGCTGTAATTCGCTATCTGCTGCTGCTG 1809
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 367 AAGTCTCCAGAGAGTGGATCAGTGCAGGCTATATTAAGTGGTAGAGAGAGGACCATAG 426
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1810 AAGGTGATCTACAAATGATAGTACTCAGAGGATTTCTTTGGGAGTTCAAAATCAAG 1869
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 427 AGATGATCTACAGAGTGTGATTCAGGCTCTCAAG-----GGCTCTGAGGCGCCGCAAG 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1870 AATGATGATGAAACAATTTACAGAGGCTATCAAGAGCTGGGCTTACAAAGATAG 1929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 ATCCAAAGAAATATCTGATCATCTCTGCTTGGAAACAGAGAGGTTCAAGAAAGATAGAG 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1930 AACCAAGAGCTACTTGAATTTCTTTGCTTGGTAAATGCTGAGATATCTGCAAGAGAA 1989
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 AGTATGAGCTCTCTAGAAA- CAGACGCGGAGATCTGATTACATACAGAGAGGCAAGAA 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1990 ATGTTTAAATGATGTAAAACTACTGAGAGAAACAAAGGCT-AGGCATCTCAATAAAGA 2049
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 598 CAGCGGTTTCATGATTTATGTCACACCAAAATGATGATGCTGACGATGATACATTA 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2050 ACCGAGATTCATGATTTATGTTTCATTCAAAAGSAAAGATAGTATGATGATATCTGT 2109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 658 TCATTGGGCTCTCAACATCAACAGAGGTCATGACGAGTGAAGGTCAGAGAGCTCTGAGATAG 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2110 TACTGGGCTCTGCAACATAAACCAGCATCATGAGAGGATCAGAGATACAGATAGAG 2169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 718 CAATGGAGTTATCAACCATCA 742
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2170 CAATGGGCTATATCAGGCTAATCA 2194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 8
US-09-878-574-9911
: Sequence 9911, Application US/09878574
: Patent No. US20020110548A1
: GENERAL INFORMATION:
: APPLICANT: Byrum, Joseph R.
: APPLICANT: Ia Kosa, Thomas J.
: APPLICANT: Thompson, Michael D.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

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? PRIOR FILING DATE: 1999-09-13
 ? PRIOR APPLICATION NUMBER: 60/161,224
 ? PRIOR FILING DATE: 1999-10-22
 ? PRIOR APPLICATION NUMBER: 60/159,878
 ? PRIOR FILING DATE: 1999-10-15
 ? PRIOR APPLICATION NUMBER: 60/157,401
 ? PRIOR FILING DATE: 1999-10-01
 ? PRIOR APPLICATION NUMBER: 60/143,419
 ? PRIOR FILING DATE: 1999-07-12
 ? PRIOR APPLICATION NUMBER: 60/143,409
 ? PRIOR FILING DATE: 1999-07-12
 ? NUMBER OF SEQ ID NOS: 196
 ? SOFTWARE: Microsoft Office 97
 ? SEQ ID NO 131
 ? LENGTH: 866
 ? TYPE: DNA
 ? ORGANISM: Zea mays

US-10-078-770-131

Query Match 10.7% Score 83.4; DB 9; Length 866;
 Best Local Similarity 58.3%; Pred. No. 9, 3e 18;
 Matches 172; Conservative 0; Mismatches 111; Indels 12; Gaps 13

QY 115 GTGGGAAAGATACATCATTCATGAGGATATCCGAAGATGCTTACATTCATGCAATGAGAC 174
 DB 97 GTGGGAAAGATGACTGATTCATGATGAGCGTGCATACAGATATGTAATGCAATGCAATGAG 156
 QY 175 GTGCTAAGGATTCATGCTAGCTGCAAAACCAAGTACTTCCTCGGAGTCTTTTCTGGG 234
 DB 157 GTGCTCAACATTCATGCTATTCATGCAACCAAGTACTTCCTCGGAGTCTTTTCTGGG 216
 QY 235 CAGCCGATGATTTACTCTGAGCAATCAATGCGCTGACCTTAATGCTGCAAAAGATTTGT 294
 DB 217 -----AATCACAATAGAGATGCTGCTGCTAATAATGCTAGCAATTCATGAGATAG 264
 QY 295 GCTGCAAGATAGTAGCAAGATTCATCAAGGAGAGAAAGTTTCAGGGGCTATGTTGCTTC 354
 DB 265 CACTGCAAAATTCGAAACAGAGATTTATTCGAATGAGAGATTTTCAGGCTTATATAGTCTC 424
 QY 435 CAATGCTGCGAGAGATTCCTCGAGAGATGGAATGCAATGCAATGCAATGCAATGCAATG 409
 DB 425 CAATGCTGCGAGAGATTCCTCGAGAGATGGAATGCAATGCAATGCAATGCAATGCAATG 479

RESULT 14

US-10-078-770-127
 ? Sequence 127, Application US/10078770
 ? Publication No. US200400471A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Fumodo, Amelayo O.
 ? APPLICANT: Forgue, Charlie
 ? APPLICANT: Miao, Guo-Rui
 ? TITLE OF INVENTION: CONAS Encoding Polypeptides
 ? FILE REFERENCE: BR-165 US NA
 ? CURRENT APPLICATION NUMBER: US/10/078,770
 ? PRIOR FILING DATE: 2002-02-19
 ? PRIOR APPLICATION NUMBER: 09/614,188
 ? PRIOR FILING DATE: 2000-07-12
 ? PRIOR APPLICATION NUMBER: 60/143,400
 ? PRIOR FILING DATE: 1999-07-12
 ? PRIOR APPLICATION NUMBER: 60/153,534
 ? PRIOR FILING DATE: 1999-09-13
 ? PRIOR APPLICATION NUMBER: 60/161,223
 ? PRIOR FILING DATE: 1999-10-22
 ? PRIOR APPLICATION NUMBER: 60/159,878
 ? PRIOR FILING DATE: 1999-10-15
 ? PRIOR APPLICATION NUMBER: 60/157,401
 ? PRIOR FILING DATE: 1999-10-01
 ? PRIOR APPLICATION NUMBER: 60/143,419
 ? PRIOR FILING DATE: 1999-07-12
 ? PRIOR APPLICATION NUMBER: 60/143,409
 ? PRIOR FILING DATE: 1999-07-12
 ? NUMBER OF SEQ ID NOS: 196

? SOFTWARE: Microsoft Office 97

? SEQ ID NO 127
 ? LENGTH: 487
 ? TYPE: DNA
 ? ORGANISM: Zea mays
 ? FEATURE:
 ? NAME/KEY: unsure
 ? LOCATION: (289)
 ? NAME/KEY: unsure
 ? LOCATION: (291)
 ? NAME/KEY: unsure
 ? LOCATION: (307)
 ? NAME/KEY: unsure
 ? LOCATION: (311)
 ? NAME/KEY: unsure
 ? LOCATION: (385)
 ? US-10-078-770-127

Query Match 10.5% Score 82.2; DB 9; Length 487;
 Best Local Similarity 59.5%; Pred. No. 1, 4e 17;
 Matches 160; Conservative 0; Mismatches 97; Indels 13; Gaps 13

QY 115 GTGGGAAAGATACATCATTCATGAGGATATCCGAAGATGCTTACATTCATGCAATGAGAC 174
 DB 87 GTGGGAAAGATGACTGATTCATGATGAGCGTGCATACAGATATGTAATGCAATGCAATGAG 146
 QY 175 GTGCTAAGGATTCATGCTAGCTGCAAAACCAAGTACTTCCTCGGAGTCTTTTCTGGG 234
 DB 147 GTGCTCAACATTCATGCTATTCATGCAACCAAGTACTTCCTCGGAGTCTTTTCTGGG 206
 QY 235 CAGCCGATGATTTACTCTGAGCAATCAATGCGCTGACCTTAATGCTGCAAAAGATTTGT 294
 DB 207 -----AATCACAATAGAGATGCTGCTGCTAATAATGCTAGCAATTCATGAGATAG 264
 QY 295 GCTGCAAGATAGTAGCAAGATTCATCAAGGAGAGAAAGTTTCAGGGGCTATGTTGCTTC 354
 DB 255 CACTGCAAAATTCGAAACAGAGATTTATTCGAATGAGAGATTTTCAGGCTTATATAGTCTC 414
 QY 435 CAATGCTGCGAGAGATTCCTCGAGAGATGGAATGCAATGCAATGCAATGCAATGCAATG 404
 DB 415 CAATGCTGCGAGAGATTCCTCGAGAGATGGAATGCAATGCAATGCAATGCAATGCAATG 444

RESULT 15

US-09-878-674-6135
 ? Sequence 6135, Application US/09878674
 ? Patent No. US2002011054A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Fumodo, Amelayo O.
 ? APPLICANT: Forgue, Charlie
 ? APPLICANT: Miao, Guo-Rui
 ? APPLICANT: Thompson, Michael D.
 ? TITLE OF INVENTION: Nucleic Acid Molecules and other Molecules Associated with
 ? FILE REFERENCE: BR-21(US401)B
 ? CURRENT APPLICATION NUMBER: US/09/878,674
 ? PRIOR FILING DATE: 2001-12-21
 ? PRIOR APPLICATION NUMBER: 09/433,536
 ? PRIOR FILING DATE: 1999-06-14
 ? NUMBER OF SEQ ID NOS: 15775
 ? SEQ ID NO 6135
 ? LENGTH: 182
 ? TYPE: DNA
 ? ORGANISM: Glycine max
 ? OTHER INFORMATION: Clone ID: Z0109784901
 ? US-09-878-674-6135

Query Match 9.7% Score 76.2; DB 10; Length 182;
 Best Local Similarity 74.8%; Pred. No. 1e 15;
 Matches 110; Conservative 0; Mismatches 49; Indels 13; Gaps 13

QY 32 CAATGCTGCGAGAGATTCCTCGAGAGATGGAATGCAATGCAATGCAATGCAATGCAATG 90
 DB 35 CAATGCTGCGAGAGATTCCTCGAGAGATGGAATGCAATGCAATGCAATGCAATGCAATG 94

Qy 92 GNTGGGAAGCGGCTGTACAGTGGGAAGATAAATCATTCATTGATAGAGTATCCAAGA 151
 | | | | |
Dd 95 GTGCCAGAGCGGACTTGTTCA-TGGGAAGATAATAATAGATCGTAGTCTCCGGA 153

Qy 152 TGGTTACATTCATGCAATCAGACGTGCTA 180
 111111 11 1111 11 111111 1
 Db 154 TGGTTATGTTAAATGCCATTGCAAGTCGGA 182

Search completed: May 5, 2003, 07:27:54
Job time : 107.12 secs


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QY 251 TCTGAGGACATCAATGCCCTGACCTTAATCCCAAGAGATTGTCGCTGAAGATAGTTAG 310
Db 1723 GCGGAAAGAAATGGTCTTCTCACTTGATTCGCAAGGAGCTCTCGCTCAAGATTCAG 1782
QY 311 CAAGATTGATCAAGGAGAGAGATTGAGGCTCTATGTTGTTGTTCCCAATGTTGGCCAGAAG 370
Db 1783 CAAGATTGAGCTGGGAGAGGCTTACTGTTTATGTTGTTGTTGTTCCCAATGTTGGCTGAGG 1842
QY 471 TCTGACAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
Db 1843 GTTCCAGAAAGCGCTTCTGTTGAGGCAATCTTGACTGCAAGGAGGAGATGATGATGAT 1902
QY 431 GATGTACAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
Db 1903 GATGTACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1962
QY 491 CTATCTGACATCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 550
Db 1963 CTATCTGACATCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2022
QY 551 TCTGTGAGAAACGAGCGGCGGACATGATTACATGAGGCGGCAAGAGGCGGCTTTTAT 610
Db 2023 AGAGGACACCGGAGGCGGACATGATTACATGAGGCGGCAAGAGGCGGCTTTTAT 2082
QY 611 GATTAGCTCCAGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670
Db 2083 GATCTATGTTTATACCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2142
QY 671 TAACATCAACGAGGCTCAATGAGCGTGCAGAGAGCTCTGATAGCAATGAGGATTA 730
Db 2143 CAACATCAACGAGGCTCAATGAGCGTGCAGAGAGCTCTGATAGCAATGAGGATTA 2202
QY 731 TCAACCATCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 783
Db 2203 CCAACCGTACCATCTGCGACTAGGAGCGCTGCGCGGCGGCGGCGGCT 2255

RESULT 6
US-08-232-463-14/c
: Sequence 14, Application US/08232463
: Patent No. 5670367
: GENERAL INFORMATION:
: APPLICANT: DORNER, F.
: APPLICANT: SCHEIFELINGER, F.
: APPLICANT: FALKNER, F. G.
: TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 1800 Diagonal Road, Suite 500
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22313-0299
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,463
: FILING DATE:
: CLASSIFICATION: 435
: PRIORITY INFORMATION:
: APPLICATION NUMBER: US/07/935,313
: FILING DATE:
: APPLICATION NUMBER: EP 91 114 300.6
: FILING DATE: 26-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Bent, Stephen A.
: REGISTRATION NUMBER: 29,768
: REFERENCE/DOCKET NUMBER: 30472/114 IMM
: TELECOMMUNICATION INFORMATION:
```

```
TELEPHONE: (703)836 9400
TELEFAX: (703)683-4109
TELEX: 894149
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7218 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: CLONE: pTZupt-Fls
US-08-232-463-14

Query Match 5.9%; Score 46.2; DB 1; Length 7218;
Best Local Similarity 3.9%; Pred. No. 6.1e-05;
Matches 15; Conservative 212; Mismatches 160; Indels 0; Gaps 0;

QY 377 AGAGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 436
Db 1428 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1369
QY 437 CAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 496
Db 1368 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1309
QY 497 GACATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 556
Db 1308 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1249
QY 557 GAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 616
Db 1248 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1189
QY 617 CGTCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 676
Db 1188 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1129
QY 677 CAACGAGAGTCAATGAGGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736
Db 1128 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1069
QY 737 ACATCACTTGTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 764
Db 1068 RRATCGCAAGCTCCCTGACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1042

RESULT 7
US-08-968-752B-5
: Sequence 5, Application US/08968752B
: Patent No. 6043073
: GENERAL INFORMATION:
: APPLICANT: Frohman, Michael A.
: APPLICANT: Morris, Andrew
: TITLE OF INVENTION: No. 6043073ei Phospholipase D Polypeptide and
: TITLE OF INVENTION: DNA Sequences
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ONYX Pharmaceuticals, Inc.
: STREET: 3031 Research Drive
: CITY: Richmond
: STATE: California
: COUNTRY: USA
: ZIP: 94806
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.40
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/968,752B
: FILING DATE: 13-AUG-1997
: CLASSIFICATION: 435
: PRIORITY INFORMATION:
```

APPLICATION NUMBER: US 60/025,469
FILING DATE: 05-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory J.
REGISTRATION NUMBER: 42,028
REFERENCE/BOOKET NUMBER: ONYX2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2799 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2799
US-09-968-752B-5

Query Match 5.7%; Score 44.8; DR 3; length 2799;
Best Local Similarity 62.5%; Pred. No. 0.0001;
Matches 70; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 610 TGATTAGTCCACACCAAAATGATCGTTGACGATGATACATATTCATTCGGCTCG 669
Db 2255 TCATCTATATCCAGGAGGATGCTATCGGATGACAGAACAGTCATGTTCTG 2414
QY 670 CTAAATCAACACAGAGTCAATGACGCGTGCAGGAGACTTTCAGATAGCAAT 721
Db 2415 CGAAATCAATGACAGGAGCTTGTGGGAGGCGTGAACTGAGCTAGCCAT 2366

RESULT 8

US-09 536-224-5
Sequence 5, Application US/04536224
Patent No. 6479665

GENERAL INFORMATION:
APPLICANT: Frohman, Michael A.
APPLICANT: Morris, Andrew
TITLE OF INVENTION: No. 6479665e1 Phospholipase D Polypeptide and
TITLE OF INVENTION: No. 6479665e1 Phospholipase D Polypeptide and
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 4031 Research Drive
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/968,752
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory J.
REGISTRATION NUMBER: 42,028
REFERENCE/BOOKET NUMBER: ONYX2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 2799 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2799
US-09 536-224-5

Query Match 5.7%; Score 44.8; DR 4; length 2799;
Best Local Similarity 62.5%; Pred. No. 0.0001;
Matches 70; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 610 TGATTAGTCCACACCAAAATGATCGTTGACGATGATACATATTCATTCGGCTCG 669
Db 2255 TCATCTATATCCAGGAGGATGCTATCGGATGACAGAACAGTCATGTTCTG 2414
QY 670 CTAAATCAACACAGAGTCAATGACGCGTGCAGGAGACTTTCAGATAGCAAT 721
Db 2415 CGAAATCAATGACAGGAGCTTGTGGGAGGCGTGAACTGAGCTAGCCAT 2366

RESULT 9

US-08 968-752B-3
Sequence 5, Application US/08968752B
Patent No. 6043074
GENERAL INFORMATION:
APPLICANT: Frohman, Michael A.
APPLICANT: Morris, Andrew
TITLE OF INVENTION: No. 6043074e1 Phospholipase D Polypeptide and
TITLE OF INVENTION: No. 6043074e1 Phospholipase D Polypeptide and
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 4031 Research Drive
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94806
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,752B
FILING DATE: 13 AUG 1997
CLASSIFICATION: 445
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,409
FILING DATE: 05 SEP 1996
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory J.
REGISTRATION NUMBER: 42,028
REFERENCE/BOOKET NUMBER: ONYX2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9758
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3108 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS

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QY 670 CTACATCAACACGAGGTCAAATGGACGGGTGCAAGAGAGACTCTGAGATAC 71H
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Db 2621 CCAACATAAATGACCGCAGCATGTGGGAAAGCGTGACAGTGAATATGCC 266H

RESULT 11
US-09-107-149-18
: Sequence 18, Application US/09107149
: Patent No. 6274364
: GENERAL INFORMATION:
: APPLICANT: Leung, David W.
: APPLICANT: Tompkins, Christopher K.
: TITLE OF INVENTION: PHOSPHATIDYLCHOLINE PHOSPHOLIPASE D
: FILE REFERENCE: 077419/0144
: CURRENT APPLICATION NUMBER: US/09/107,149
: CURRENT FILING DATE: 1998-06-30
: EARLIER APPLICATION NUMBER: 08/768,147
: EARLIER FILING DATE: 1996-12-17
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 3114
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (52)..(2964)
US-09-107-149-18

Query Match 5.38; Score 41.8; DB 4; Length 3114;
Best Local Similarity 61.58; Pred. No. 0.0011;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps

QY 610 TGATTTCATCCACACCAAAATGATGATCGTTGACGATGAATACATATCATTTGGGTCTG 669
      ||| ||||| || | | | | | | | | | | | | | | | | | | | | |
Db 2726 TTATCATGTCACACAGCAAGTTGTTAAATGGCTGATGAACACTGTATATTGGTCTG 2785H

QY 670 CTACATCAACACGAGGTCAAATGGACGGGTGCAAGAGAGACTCTGAGATAC 71H
      ||||| || | | | | | | | | | | | | | | | | | | | | |
Db 2786 CCAACATAAATGACCGCAGCATGTGGGAAAGCGTGACAGTGAATATGCC 284H

RESULT 12
US-08-968-752B-1
: Sequence 1, Application US/08968752B
: Patent No. 6043073
: GENERAL INFORMATION:
: APPLICANT: Frohman, Michael A.
: APPLICANT: Morris, Andrew
: TITLE OF INVENTION: No. 6043073ol Phospholipase D Polypeptide and
: TITLE OF INVENTION: DNA Sequences
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ONYX Pharmaceuticals, Inc.
: STREET: 3031 Research Drive
: CITY: Richmond
: STATE: California
: COUNTRY: USA
: ZIP: 94806
: COMPUTER READABLE FORM:
: MEDIUM TYPE: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.40
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/968,752B
: FILING DATE: 13-AUG-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/025,469
: FILING DATE: 05 SEP-1996
: ATTORNEY/AGENT INFORMATION:

```

```

: NAME: Giotta, Gregory J.
: REGISTRATION NUMBER: 42-02H
: REFERENCE/DOCKET NUMBER: 08VX2004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 510-222-9700
: TELEFAX: 510-222-9758
: INFORMATION FOR SEQ ID NO: 1:

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? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..4222
US-08-968-752B-1

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Query Match	5.4%	Score	41.8	DB	3	Length	4222
Best Local Similarity	61.5%	Prod. No.	0.0011				
Matches	67	Conservative		Mismatches	42	Indels	Gaps
QY	610	TCATTACGTCACACCAAAATGATGATCGTTGACGATCAATATCATATGGGCTCTG	669				
DB	2675	TTATCTATGTCACACGCAAGTTGTTTAATCTCTATATATACACATGTTATTATGGCTCTG	2744				
QY	670	CTAATCATCAACCAATATGTCATATGACGATGGCTGCACAGCACTCTGAGATAGC	718				
DB	2735	CCAACTATAATTCAGACGATCATGCTGGCAAGGCTTCACATCTAAATGGC	2783				

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1  RESULT 14
2  US 09 536-224-1
3  : Sequence 1, Application US/09546224
4  : Patent No. 6379665
5  : GENERAL INFORMATION:
6  : APPLICANT: Frohman, Michael A.
7  : APPLICANT: Morris, Andrew
8  : TITLE OF INVENTION: No. 6379665e1 Phospholipase D Polypeptide and
9  : TITLE OF INVENTION: DNA Sequences
10 : NUMBER OF SEQUENCES: 8
11 : CORRESPONDENCE ADDRESS:
12 : ADDRESSEE: ONYX Pharmaceuticals, Inc.
13 : STREET: 401 Research Drive
14 : CITY: Richmond
15 : STATE: California
16 : COUNTRY: USA

```

```

1 SURVIVABILITY: double
2 TOPOLGY: linear
3 MOLECULE TYPE: cDNA
4 HYPOTHETICAL: NO
5 ANTI-SENSE: N
6 FEATURE:
7
8 NAME/KEY: CDS
9 LOCATION: 1..4222
10 DS-09-546-224-1

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	Query Match	5.98;	Scores	41.18;	DG	4;	LocusID	42227
	Best Local Similarity	61.9%	Fred.	No.	0.0011;			
	Matches	67;	Conservative	0;	Mismatches	42;	Inhibits	0;
QY	610	TGAATTAGTCTCACCACAAATCATGTTCATAAAGAATCAATTAATTTATTTGGTGCG	639					
UB	2675	TTAICTATGTCTCCACGAAACTGTCTTAATCTTGAATGAIAANATCTGATTAATATTTGCCT	2744					
QY	670	CTAAATATCAACGACAGCTCACATGCCCTCTTAATCAATATCTGTCAATATATCT	710					
b	2785	CACACAATAAAAGAACGATATCTGAAAAAGAGATGAAATGAAAAATGAG	2798					

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1  RESULT 14
2  US 09/141-206, 1
3  : Sequence 1, Application US/00141206,
4  : Patent No. 6187559
5  : GENERAL INFORMATION:
6  : APPLICANT: Stodd, Paul M.
7  : APPLICANT: Laszlo, Daniel J
8  : TITLE OF INVENTION: Amino Acid Sequence 6
9  : Patent No. 6187559
10 : FILE REFERENCE: 4 30148/01/03/1954/R
11 : CURRENT APPLICATION NUMBER: US/09/141, 206
12 : CURRENT FILING DATE: 1998 08 27
13 : EARLIER APPLICATION NUMBER: 60/057,802
14 : EARLIER FILING DATE: 1997 08 28
15 : NUMBER OF SEQ ID NOS: 8
16 : SOFTWARE: Patent In Ver. 2.0
17 : SEQ ID NO 1
18 : LENGTH: 4400
19 : TYPE: DNA
20 : ORGANISM: Human
21 : FEATURE:
22 : NAME/KEY: CDS
23 : LOCATION: (162)..(2963)
24 : OTHER INFORMATION: Human P112
25 : US 09 141-206, 1

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[illegible]

RESULT 15:
US-09/107 149 16
: Sequence 16, Application DS/09/01/149
: Patent No. 6274464
: GENERAL INFORMATION:
: APPLICANT: Lempi, David W.
: APPLICANT: Lempi, David W.
: TITLE OF INVENTION: PROSODY-DRIVEN
: FILE REFERENCE: 072419/0144
: CURRENT APPLICATION NUMBER: US/09/107 149
: CURRENT FILING DATE: 1998 09 30

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? EARLIER APPLICATION NUMBER: 08/768,147
? EARLIER FILING DATE: 1996-12-17
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 16
? LENGTH: 3425
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (64)..(2862)
US-09-107-149-16

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Query Match      5.2%; Score 41; DB 4; Length 3425;
Best Local Similarity 60.2%; Pred. No. 0.0022;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 610 TGATTTACGTCACACGCAAAATGATGATGTTGACGATGAATACATTATTCATTGGGTCTG 669
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2318 TCATCTACATCCACAGCAAGTGCTCATGCGCAGATGACGGGACAGTCATCATTGTTCTG 2377
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 670 CTACATCAACACAGAGCTCAATGCGGTTGCAAGACATCTCGAGATAGCAATG 722
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2378 CAACATCAATGACGGGAGCTTGCTGGGAGCGGGACAGTGAGCTGSCCGTG 2430
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Search completed: May 5, 2003, 07:31:46
Job time : 72.7368 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleotide - nucleic search, using sw model

Run on: May 4, 2003, 21:54:51 ; Search time 203,554 Seconds
(without alignments)
8658,379 Million cell updates/sec

Title: US-09-817-869-1
Perfect score: 783
Sequence: 1 ttttccaaqaccacacatg.....tcgtggccagatccatggt 783

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1:	/SID52/qcdata/geneseq/geneseq-emb1/NA1980.DAT:*						
2:	/SID52/qcdata/geneseq/geneseq-emb1/NA1981.DAT:*						
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4:	/SID52/qcdata/geneseq/geneseq-emb1/NA1983.DAT:*						
5:	/SID52/qcdata/geneseq/geneseq-emb1/NA1984.DAT:*						
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8:	/SID52/qcdata/geneseq/geneseq-emb1/NA1987.DAT:*						
9:	/SID52/qcdata/geneseq/geneseq-emb1/NA1988.DAT:*						
10:	/SID52/qcdata/geneseq/geneseq-emb1/NA1989.DAT:*						
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12:	/SID52/qcdata/geneseq/geneseq-emb1/NA1991.DAT:*						
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19:	/SID52/qcdata/geneseq/geneseq-emb1/NA1998.DAT:*						
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21:	/SID52/qcdata/geneseq/geneseq-emb1/NA2000.DAT:*						
22:	/SID52/qcdata/geneseq/geneseq-emb1/NA2001A.DAT:*						
23:	/SID52/qcdata/geneseq/geneseq-emb1/NA2001B.DAT:*						
24:	/SID52/qcdata/geneseq/geneseq-emb1/NA2002.DAT:*						

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	535.6	68.4	1062	ABN98376	Arabidopsis thalia
2	478.4	61.1	2834	AAI88222	Castor bean Phosph
3	445.8	56.9	3040	AAQ86783	DNA encoding Phosp
4	445.8	56.9	3040	AAI42853	Phospholipase D pr
5	445.8	56.9	3040	AAI85509	Phospholipase D en
6	425	54.3	2708	AAQ86784	DNA encoding Phosp
7	217.2	30.3	551	AAH50935	Lipid degradation
8	217.2	30.3	551	AAH56942	p patens lipid met
9	191.6	24.5	1997	AAC47118	Arabidopsis thalia

10	191.6	24.5	1216	21	AAC42946	Arabidopsis thalia
11	173.8	22.2	641	22	AAH50934	lipid degradation
12	173.8	22.2	641	22	AAH56941	p patens lipid met
13	103.6	13.2	833	24	ABN98920	Arabidopsis thalia
14	97.8	12.5	452	24	ABL93878	Arabidopsis thalia
15	95.4	12.2	1173	22	AAH21721	Tobacco phospholip
16	91.2	11.6	639	22	AAH50936	Lipid degradation
17	91.2	11.6	639	22	AAH56943	p patens lipid met
18	47.8	6.1	1070	24	ABN98366	Arabidopsis thalia
19	45	5.7	4434	23	ABL19571	Protophila melanoq
20	45	5.7	4497	23	ABL19569	Protophila melanoq
21	45	5.7	14245	23	ABL03938	Protophila melanoq
22	45	5.7	15238	23	ABL19570	Protophila melanoq
23	45	5.7	15243	23	ABL19568	Protophila melanoq
24	44.8	5.7	2799	19	AAV20871	Murine phospholipa
25	44.8	5.7	3374	19	AAV20872	Murine phospholipa
26	41.8	5.3	3108	19	AAV20869	Human phospholip
27	41.8	5.3	3114	21	AAZ49971	Human phosphatidyl
28	41.8	5.3	3114	22	AAH47447	Human phosphatidyl
29	41.8	5.3	3222	19	AAV20867	Human phospholipas
30	41.8	5.3	3495	19	AAV20870	Human phospholipas
31	41.8	5.3	3609	19	AAV20868	Human phospholipas
32	41.8	5.3	3609	24	AAH59518	Human phospholipas
33	41.8	5.3	3620	22	AAH98437	Human EST-derived
34	41.8	5.3	3703	23	AAH81114	DNA encoding novel
35	41	5.2	3388	22	AAH62680	Human phospholipas
36	41	5.2	3425	21	AAZ49970	Human phosphatidyl
37	41	5.2	3425	22	AAH47446	Human phosphatidyl
38	39.4	5.0	3425	20	AAV99778	Human phosphatidyl
39	39.4	5.0	3425	21	AAZ49969	Human phosphatidyl
40	39.4	5.0	3425	22	AAH47436	Human phosphatidyl
41	37.6	4.8	5727	24	AAS20500	Expression vector
42	37.6	4.8	6757	24	AAS20498	Expression vector
43	37.6	4.8	8272	24	AAS20499	Expression vector
44	36.2	4.6	7256	24	AAS20505	Expression vector
45	36.2	4.6	7639	24	AAS20503	Expression vector

ALIGNMENTS

RESULT 1

ABN98376

ID ABN98376 standard; DNA; 1062 BP.

AC ABN98376;

DT 01-AUG-2002 (first entry)

DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 144.

KW Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
KW disease; crop; thale cress; tolerance factor; insect; pathogen;
KW nutrition; ds.

OS Arabidopsis thaliana.

PN US2002023281-A1.

PP 21-FEB-2002.

PR 26-JAN-2001; 2001US-0770445.

PR 27-JAN-2000; 2000US-178472P.

XX (GORL/) GORLACH J.

XX (ANY/) AN Y.

XX (HAMI/) HAMILTON C M.

XX (PRIC/) PRICE J L.

XX (RAIN/) RAINES T M.

XX (YUY/) YU Y.

XX (RAME/) RAMEKA J G.

XX (PAGE/) PAGE A.

PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD H L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRICK/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX
PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Ramezani JG, Page A, Mathew AV, Ledford HL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
DR WPI: 2002 400781/43.
XX
XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of protein
XX
XX Claim 1: SEQ ID NO 144; 49pp + Sequence Listing; English.
XX
XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridizing under stringent conditions
CC to a sequence selected from any one of 999 sequences (A8N98233-A8N99231),
CC given in the specification or its fragment. A polypeptide (II) encoded by
CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
CC useful for screening a candidate agent for its biological effect. (I) is
CC useful in identifying homologous or related genes, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, mapping functional regions of the protein and in studying
CC associated physiological pathways. (I) is also useful for the genetic
CC manipulation of cells, particularly plant cells. (I) is also useful in
CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful
CC for enhancing or inhibiting production of a biosynthetic product in a
CC plant. (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docID=999909770445.
XX
XX Sequence 1062 BP; 286 A; 247 C; 251 G; 288 T; 0 other;
XX
XX Query Match 68.4%; Score 545.6; DR 24; Length 1062;
XX Best Local Similarity 97.5%; Prod. No. 1.1e-161;
XX Matches 544; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
XX 226 TTGCTTGGGACGACGATGATTAATCTGAGGACATCAATGGCTGCACCTTAATGCCAA 285
XX 1 TTGCTTGGGACGACGATGATTAATCTGAGGACATCAATGGCTGCACCTTAATGCCAA 60
XX
XX 286 AAGAGCTGTCTGCTGAAGATATTAAGATTAATCAAGGAGACAGCACTTCAGGCTCATG 445
XX
XX

DB 61 AAGAGCTGTCTGCTGAAGATATTAAGATTAATCAAGGAGACAGCACTTCAGGCTCATG 120
QY 446 TTGCTTGGGACGACGATGATTAATCTGAGGACATCAATGGCTGCACCTTAATGCCAA 405
DB 121 TTGCTTGGGACGACGATGATTAATCTGAGGACATCAATGGCTGCACCTTAATGCCAA 180
QY 406 ACTGCGAG 465
DB 181 ACTGCGAG 240
QY 466 TTGAGGCGCGCGAG 525
DB 241 AAGCGTCCTGAG 300
QY 526 TCAAGGAG 585
DB 401 TCAAGGAG 460
QY 586 GCGCGGAG 645
DB 461 GCGCGGAG 420
QY 646 ATGAATACATTAAT 705
DB 421 ATGAATACATTAAT 480
QY 706 ACTCTGAGATAG 765
DB 481 ACTCTGAGATAG 540
QY 766 GTGCGGAG 825
DB 541 GTGCGGAG 600
XX
XX RESULT 2
XX AAT88222
XX ID AAT88222 standard; cDNA to mRNA; 2834 BP.
XX AC AAT88222;
XX 19-JAN-1998 (first entry)
XX Castor bean phospholipase B cDNA.
XX
XX Castor bean phospholipase B; hydrolysis; phospholipid; product ion;
XX phosphatidic acid; transphosphatidyl derivative; endosperm; etc.
XX
XX Ricinus communis.
XX
XX Key Location/Qualifiers
XX CDS 172..2598
XX /cds
XX /product phospholipase B
XX
XX D55670366 A.
XX
XX 24-SEP-1997.
XX
XX 06-JUN-1996; 9508 0471251.
XX
XX 06-JUN-1996; 9508 0471251.
XX
XX (UNIV) UNIV KANSAS STATE RES FOUNDR.
XX
XX Wntq X;
XX
XX WPI: 1997 479462/44.
XX
XX P PSDB; AAW42911.
XX
XX Recombinant Ricinus communis phospholipase B gene, which hydrolyses
XX phospholipid(s) to produce phosphatidic acid and transphosphatidyl
XX derivatives

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XX Claim 6: Columns 11-14; 14pp: English.
XX The present sequence encodes castor bean phospholipase D (PLD),
CC which hydrolyses phospholipids to produce phosphatidic acid and
CC transphosphatidyl derivatives.
CC A lambda zap cDNA library from castor bean endosperm was screened
CC with PLD cDNA specific probes. Clones that hybridised with both
CC probes were excised in vivo with helper phage R344 in phagescript
CC SK(-). Both ends of the inserts were sequenced. The deduced amino
CC acid sequence from 1 clone matched the amino-terminal sequence of
CC purified Ricinus communis PLD.
XX
SQ Sequence 2834 BP; 815 A; 550 C; 668 G; 801 T; 0 other;
  Query Match      61.1%; Score 478.4; DB 18; Length 2834;
  Best Local Similarity 78.1%; Pred. No. 5e-143;
  Matches 600; Conservative 0; Mismatches 166; Indels 2; Gaps 2;
  17 GATGTGTGGAATGTCGAATGTTTAAAGTCCATTGATGGAGGAGCTCTCTGGTTTCCC 76
  1542 GAGGCAATGGAATGTCAGTTGTTAGATCCATTGATGGTGGAGCTGCATTGGTTCCCT 1601
  77 GACTGCCCTGAAGCTGCTGCGGAAGCCGGCTTGACATGGAAGATAACATCATTCGA 136
  1602 GACACACCTGAAGATGCGGCAGAGGCTGGGCTTGACATGGAAGATAACATCATTCGA 1661
  137 TAGGATATCCAAAGATGCTTACATTCATCAATCAGATGCTGTAAGGATTTTCATAGT 196
  1662 CCGAAGATATTC-AGATGCTTTATATCCATGCCATTCGAAGGGCAAGAATTTATATAT 1720
  197 TGAAGAACAGTACTTCCTGGAGTTC-TTTTGCTTGGCCAGCCGATGTTACTTCCTG 255
  1721 TGAAGATCAATTCCTTGGAGTTCCTTTTGGTGGAGTCTCTGATGGTATTACCCCTG 1780
  256 AGGACATCAATGCCCTGCACCTTAATCCCAAGAGTTCCTGTAAGATAGTTAGCAAGA 315
  1781 AGGATATTATGCACTGCTCATTAATAGCAAGGAACCTTCACCTCAAGTACTTAGCAAGA 1840
  316 TTGATCAAGSAGAGAGTTCAGGCTTAAGTTGTTGGTCCCATCTGGCCAGAGGCTCTCC 375
  1841 TTCCGGCAGGGAGAGGTTTCACTGTTTACATGTTTGTTCATATGTTTCCCATGTTGGCCAGAGGATATAC 1900
  376 CAGAGAGTGGATCAGTGTCAAGCTATATTAGCTGGCAGAGGAGGACCATGGAGATGATG 435
  1901 CAGAGAGTGCATCACTTACGGCTATATTAGATTGCCAGAGAGGACATGGGAATGATGT 1960
  436 ACAAGATGTGATTCAGGCTCTCAAGGGTCTTTAGGGCCCGGGAAGATCCCAAGAACTATC 495
  1961 ATAAGATATTGTGCAAGGCTCTCAAGGCCAATGGAATTATTGAGGATCTCGGAATATC 2020
  496 TGACATCTCTCTGCTTGTGAACCGTGAGGTCAAGAAAGATGAGAGATAGAGCTGTG 555
  2021 TGACATCTCTCTGCTTGTGAACCGTGAGGTCAAGAAAGATGAGTGTGAATATGAACCTGCAG 2080
  556 AGAAATCAGACCCGACATGATTACATGAGGGCCGCAAGACGACGCGCTTCATGATTT 615
  2081 AAAAAACGAGGCTGATACAGACTATATAAGAGCTCAGAGGCCAGAGCTTTCATGATTT 2140
  616 AGCTCCACACCAAAATGATGCTGTTGACGATGAATATCATTTATCATTTGGTCTGCTAACA 675
  2141 ATGTTATACAAGAATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 2200
  676 TGAACAGAGGTCATTTGAGACGGTGGCAAGAGACTCTGAGATAGCAATGGAGGTTATCAAC 735
  2201 TGAACAGAGATCAATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 2260
  736 CACATCACTTTGCCATACAGAACGAGCTCTGTCGTCAGATCCATGCT 783
  2261 CACATCACTTTGCCATACAGAACGAGCTCTGTCGTCAGATCCATGCT 2308
  RESULT 3
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XX claim 9; Page 24-29; 41pp; Japanese.
XX The DNA encodes a plant derived phospholipase D (PLD). The PLD is
XX useful for measuring phospholipid levels and for producing derivs.
XX by e.g. base exchange reactions. DNA controlling the expression of
XX the plant derived PLD is also claimed and shown in AA046785.
XX Sequence 2708 BP; 646 A; 709 C; 774 G; 589 T; 0 other;
Query Match: 54.3%; Score 425; DB 16; Length 2708;
Best Local Similarity 72.7%; Pred. No. 7, 6e-126;
Matches 562; Conservative 0; Mismatches 210; Indels 1; Gaps 1;
DB 11 GACGACGAGTGTGCAATGTCTCAATTTGTTAAGTCCATGAGAGAGTCTCTCTGAG 70
DB 1388 GACAGAGACATGAAATGTTTCAGTCTTTCAGATCCATGATGTTGCTGCTTTGGC 1447
QY 71 TTTCGGAGTCCCTGGAAGCTGCTGGGAGCCGGCTTGACATGGGAAAGATAACAT 130
DB 1448 TTCCCGGAGCTCCGAGAGAGCTGCAAGAGCTGGGCTTGT-GAGTGGAAAGATCAAT 1506
QY 131 CATTGATAGAGATATCCCAAGATGCTTACATTATCATCAATACAGAGCTGCTAAGGATTTTCA 190
DB 1507 CATGACAGGAGTATCCAGGATGATACATACGTAACGCTATACGAGCGGGAAGACATTCAT 1566
QY 191 CTAGCTGAAAGACATGCTGCTGGGAGTCTTTGCTTGGGACAGGATGATGATTATG 250
DB 1567 CTACATTGAGAAATCAGTACTGTTTGGAAAGTTTATACGCTGGGAGGCGGAGAGCATGAA 1626
QY 251 TCTGAGGACATCAATGCTGCTCACTTAATGCAAAAGTGTGCTGGAAGATAGTTAG 310
DB 1627 GCGGCAAAATCGCTGCTTCACTTTCATTCGTAAGAGCTGCTGCTGGAAGATTTGCTAG 1686
QY 311 CAAATGATCAAGAGAGAGATCTCAGGCTCTATGCTTGTCTTCAATGTGCGCAGAGG 370
DB 1687 CAAGATCAAGCTGGGAGCGGTTTACTGTTTATGTTGCTGCTCAATGTGCGCTGAGGG 1746
QY 471 TCTGCAAGAGTGAATCAATGCAAGCTATATTGACTGGGAGAGAGATGATGAGAT 430
DB 1747 TGTTCGAAAGAGCTGCTGCTGCAAGCTAATGCTGCAAGAGAGAGATGAGAT 1806
QY 431 GATGTAAGAGTGTGATGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGAA 490
DB 1807 GATGTAAGTCAATGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGA 1866
QY 491 CTATGCAATGCTGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCA 550
DB 1867 CTATGCAATGCTGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCA 1926
QY 551 TCTGCAAGAGTGAATCAATGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCA 610
DB 1927 AGAGGAGTCAATGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTT 1986
QY 611 GATTGATGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCA 670
DB 1987 GATGTAAGTCAATGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTT 2046
QY 671 TAATCAATGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCA 730
DB 2047 CAACATCAACGAGAGTCCATGAGGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCA 2106
QY 731 TCAACCAATCAATGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCA 783
DB 2107 GAGGCGTACCACTTGGTGAAGTGGCTGCTGCAAGCTGCTGCAAGCTGCTGCAAGCTGCTGCA 2159
RESULT 7
AAH50945
DB AAH50945 standard; cDNA: 551 BP.
XX
AC
XX

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DB 28 AUG 2001 (first entry)
XX Lipid degradation protein encoding nucleotide sequence #10.
XX Mass: Physcomitrella patens; Lipid metabolism related proteins; LMPs;
XX Lipid biosynthesis; Lipid modification; Lipid degradation; Enzymes;
XX Fatty acid transport; Gene expression; Fatty acid; Enzyme; Plant;
XX Microorganism; Polyunsaturated fatty acid; Oilseed plant; Maize; Wheat;
XX Biotic stress tolerance; Abiotic stress tolerance; Yeast; Oil; Trifolium;
XX Pepper; Sunflower; Rapeseed; Cotton; Tobacco; Equatorial; Tomato; Vicia;
XX Pea; Alfalfa; Coffee; Carrot; Tea; Salix; Oil palm; Coconut;
XX Perennial grass; Tobacco crop; ss.
XX Physcomitrella patens.
XX W200148484 A2.
XX 31-MAY-2001.
XX 22 NOV-2000; 2000W0-EP1415.
XX 25 NOV 1999; 5960 EP09108.
XX (HAB1) BASF PLANT SCI GMBH.
XX Leibel J, Benz A, Ehrhardt T, Reinold A, Cirpus P, Hirschfeld P,
XX Frank M, Freund A, Imwong E, Schmidt K, Reisk K.
XX W01: 2001 467669/40.
XX Nucleotide acids encoding lipid metabolism related proteins from
XX Physcomitrella patens useful to produce time chemicals in modified
XX organisms, particularly polyunsaturated fatty acids in oilseed plants
XX Claim 7: Page 98; 120pp; English.
XX The present invention describes isolated nucleotide acid sequences which
XX encode lipid metabolism related proteins (LMPs). The LMP nucleotide acids
XX can be used to modify lipids and fatty acids, cofactors and enzymes in
XX microorganisms and plants, particularly to produce polyunsaturated fatty
XX acids, and are especially useful in oilseed plants. The nucleotide acids
XX may also confer biotic or abiotic stress tolerance, particularly to
XX maize, wheat, rice, oil, trifolium, tea, barley, soybean, peanut,
XX cotton, rapeseed, canola, mandarin, pepper, sunflower, tobacco, potato,
XX tobacco, eggplant, tomato, Vicia species, pea, alfalfa, coffee, carrot,
XX tea, Salix species, oil palm, coconut, perennial grasses and forage
XX crops. AAH50882 to AAH50968 represent primers used in the amplification
XX of the present invention. AAH50883 to AAH50968 represent LMP nucleotide
XX sequences, and AAH50883 to AAH50928 represent LMP protein sequences.
XX given in the present invention.
XX Sequence 551 BP; 169 A; 115 C; 142 G; 125 T; 0 other;

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Query Match: 40.0%; Score 237.2; DB 22; Length 551;
Best Local Similarity 67.5%; Pred. No. 5, 4e-66;
Matches 370; Conservative 0; Mismatches 163; Indels 15; Gaps 2;
QY 103 CGGCTGTGACAGTGGCAAGATGAAATATGATATGATATGATATGATATGATATGATATG 162
DB 16 CAGCTTTCACAGTGGTGAAGATGAAATATGATATGATATGATATGATATGATATGATATG 75
QY 163 ATGCAATGCAAGCTGTAAGATTTGATATGATATGATATGATATGATATGATATGATATG 222
DB 76 AGGCTATGCAAGTGGTGAAGATTTGATATGATATGATATGATATGATATGATATGATATG 145
QY 223 GTTGTGTGAGGAGGAGATGATATGATATGATATGATATGATATGATATGATATGATATG 282
DB 146 GTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 185
QY 283 CAAAGAGATGCTGCTGCAAGATGATATGATATGATATGATATGATATGATATGATATGAT 442
DB 184 CCAAGAGATGCTGCTGCAAGATGATATGATATGATATGATATGATATGATATGATATGAT 443

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Matches	370;	Conservative	0;	Mismatches	163;	Indels	15;	Gaps	2;
QY	103	CGCGGTTGACAGTGGCAAGATCAACATCATTTAGACGATATGCAAGATGCTATATC	162						
DB	16	CAGTTTCACAAAGTGGTAAGAAACAACACCATTCAGCGTAGTATCCAGATGGGTATAC	75						
QY	163	ATGCAATCAGACGTCGCTAAAGATTTTCATCTAGCTTGAACACGATCTCTCTGGAGTT	222						
DB	76	ACGCCATTAGACGTCGCAAGATTTTCATCTACATGAAACACATATCTCTTAGAGAGTT	145						
QY	223	CTTTGCTTGGCGACGCGATGATATACCTCTGAGGAATACAAAGCTGCTGACTTAATCC	282						
DB	136	GCTATGTCATGGAGTGAAGA-----CCAGATGCGGCTGCTTCTTCAACAATCC	183						
QY	283	CAAAAGAGTTGGCTGAAGATAGTTACCAAGATGATCAAGSAGAGAAATTCAGGCTCT	342						
DB	184	CCATCGAGCTCACAAAGAAAGATCTTAAGCAAAATTGAAGATGGAGAGAGGTTTTCAT	243						
QY	343	ATGTTGTTGCTGCAATGTCGAGAGAGTCTCCAGAGATGAGATGATGATGAGTAACTATAT	402						
DB	244	ACGTGCTGCTACCCATGTGGCTGAAGGATATCGGAAAGTGTCTGTGTAAGCTATCC	303						
QY	403	TAGACTGGCAGAGAGGACCATGGAGATGAGTAATAGAGATGTCATTAAGCTCAAGG	462						
DB	304	TAGACTGGCAGAGAGGACCATGGAGATGAGTAATAGAGATGTCATTAAGCTCAAGG	363						
QY	463	GTC---TTGAGGGCGCGAAGATCCAGAAACTATCATGATCTCTCTCTGCTGCAAGC	519						
DB	364	CTCAAGGATATCGAGATCAAGTCCCAAGGATTTATCATTTCTTCTTGGCAATA	423						
QY	520	GTGAGTCAAGAAAGATGGAGATGATGAGCTGCTGAGAAACAGAGCCCGACACTGAT	579						
DB	424	GATGAGCAAGAGTATGAGGGGGAATATGACCTACTGAGCCCGAGAGGAGCAAT	483						
QY	580	ACATGAGGGCGCAAGAGAGCGCTTTTCATGATTTACGTCCACACCAAAATGATGCG	639						
DB	484	ATGAGTCTGCTCAAGCGGCTCGGCGATTTATGATCTACGTGTCATTCGAATTCATGATG	543						
QY	640	TTGACGAT 647							
DB	544	TGATGAT 551							
RESULT 9									
ID	AAC47118	standard;	DNA;	1997	BP.				
XX	AAC47118;								
AC	AAC47118;								
DT	18-OCT-2000	(first entry)							
DE	Arabidopsis thaliana	DNA fragment	SEQ ID NO:	52628.					
XX	Hybridisation assay;	genetic mapping;	gene expression	control;					
KW	protein identification;	signal transduction	pathway;						
KW	metabolic pathway;	promoter;	termination	sequence;	ss.				
XX	Arabidopsis thaliana.								
XX	EP1033405-A2.								
PN	06-SEP-2000.								
XX	25-FEB-2000;	2000EP-0301439.							
XX	25-FEB-1999;	990S-0121H25.							
PR	05-MAR-1999;	990S-0123180.							
PR	09-MAR-1999;	990S-0123548.							
PR	23-MAR-1999;	990S-0125788.							
PR	25-MAR-1999;	990S-0126264.							
PR	29-MAR-1999;	990S-0126785.							
PR	01-APR-1999;	990S-0127462.							
PR	06-APR-1999;	990S-0128234.							

QY	343	ATGTTGTTGTTTCAATGTCGCAAGAGTCTCCGACAGAGTGCATCAGTCAAGCTATAT	402																															
DB	244	ACGTTGGTACCATGTGCTCAAGGTATCCGAAAGTGGCTCGGTCGAAGCTATCC	303																															
QY	403	TAGACTGGCAGAGAGGACCATGGAGATGATGATACAAAGATGTCAGGCTCTCAAGG	462																															
DB	304	TAGACTGGCAGAGAGGACCATGGAGATGATGATACAAAGATGTCAGGCTCTCAAGG	363																															
QY	463	GTC---TTGAGGGCCCGGAGATCCAGAACTATCIGACATTTCTTCTTGGAAACC	519																															
DB	364	CTCAAGTATCGAGATCAAGTCCCAAGGATTTATCATTTCTTCTTGGCAATA	423																															
QY	520	GTGAGGTCAAGAAAGATGGAGATGATGAGCTGCTGAGAAACAGAGCCCGACACTGAT	579																															
DB	424	GATGAGCAAGAGTATGAGGGGGAATATGACCTACTGAGCCCGAGAGGAGCAAT	483																															
QY	580	ACATGAGGGCGCAAGAGAGCGCTTTTCATGATTTACGTCCACACCAAAATGATGCG	639																															
DB	484	ATGAGTCTGCTCAAGCGGCTCGGCGATTTATGATCTACGTGTCATTCGAATTCATGATG	543																															
QY	640	TTGACGAT 647																																
DB	544	TGATGAT 551																																
RESULT 8																																		
AAH56942																																		
ID	AAH56942	standard;	cDNA;	551	BP.																													
XX	AAH56942;																																	
DT	06-SEP-2001	(first entry)																																
DE	P patens	lipid metabolism related protein coding sequence #69.																																
XX	Moss;	LMPB;	lipid metabolism related protein;																															
XX	fine chemical;	transgenic plant;	ss.																															
OS	Physcomitrella	patens.																																
XX	W02001J8541-A1.																																	
XX	31-MAY-2001.																																	
XX	25-NOV-1999;	99W0-EP09108.																																
XX	25-NOV-1999;	99W0-EP09108.																																
XX	(BADI)	BASE PLANT SCI	GMFH.																															
XX	Lerchl J.,	Renz A.,	Ehrhardt T.,	Reinold A.,	Cirpus P.,	Bischoff F.,																												
XX	Frank M.,	Freund A.,	Dowenig E.,	Schmidt R.,	Reski K.,																													
XX	WPI:	2001-381293/40.																																
XX	New isolated	nucleic acid molecule	encoding lipid	Metabolism	Related																													
XX	Proteins	useful in the	production of	tine chemicals	-																													
XX	Claim 7:	Page 95;	113pp;	English.																														
XX	The present	invention	provides	the	protein	and	coding	sequences	of	a																								
XX	number	of	moss	lipid	metabolism	related	proteins	(LMPs).	The	moss																								
XX	Physcomitrella	patens	is	one	of	the	few	plants	able	to	produce																							
XX	polynaturated	fatty	acids,	and	the	sequences	can	be	used	to	create																							
XX	transgenic	plants	also	capable	of	producing	them.	They	can	also	be																							
XX	to	identify	the	presence	of	P. patens	and	in	the	production	of																							
XX	chemicals.	The	present	sequence	is	one	of	the	conas	of	the																							
XX	Sequence	551	BP;	169	A;	115	C;	142	G;	125	T;																							
XX	Query Match	30.38;	Score	237.2;	DB	22;	Length	551;																										
XX	Best Local Similarity	67.58;	Pred.	No.	9.4e-66;																													

QY	103	CGGGCTTGCTACACTGGGAAGATAACATCATTTAGATAGAGATGATCCAAAGATGATATC	162
DB	16	CAGTTTTCACAGTGGTAAGAACACACCATTCACCGTAGTATCCAGGATGGGTATCA	75
QY	163	ATGCAATCAGCTGCTTAAGATTTTCATGTAGCTTGAATTCAGATCTTCTGAGAT	222
DB	76	ACGCCATTAGACCTGCAAGATTTTCATGTACATTCAAAAGTACTTCTTAGGAGT	135
QY	223	CTTTTCTTGGCAGCGGATGATTTATCTCTTCTGAGATATCAATGCTCTGACTTAA	282
DB	136	GGTATGCTGGAGTGAAGG-----GCAAGATGCTGCTTCTTCTGAGATGCT	183
QY	283	CAAAAGATGCTGCTGGAAGATAGTTAGCAAGATTCATCAAGGAGAGATTCAGGCT	442
DB	184	CCAUGGAGCTCACAAAGATGCTGAAGTAAATTCAGATGAGAGAGATTTGAGAT	243
QY	343	ATGTTGCTGCTCAATGTGCTGAGAGATTTCTCTGATGATGATGATGATGATGAT	402
DB	244	ACGTTGCTGCTACCATGCTGCTGAGGATATTCGCAAGATGCTGCTGCTGCTGCT	303
QY	403	TAGACTGGCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT	462
DB	304	TAGACTGGCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT	363
QY	463	GTC---TTGAGGGCGGAGAGATGCAAGAACTATCTGATCTCTTCTGAGAAAC	519
DB	364	CTCAAGTATCGAGATCAAGTCTCAAGGATTTATCATTTCTTCTTGGCAATA	423
QY	520	GTGAGGTCAAGAAAGATGGAGATGATGAGCTGCTGAGAAACAGAGCCCGACACT	579
DB	424	GATGAGCAAGAGTATGAGGGGGAATATGACCTACTGAGCCCGAGAGGAGCAAT	483
QY	580	ACATGAGGGCGCAAGAGAGCGCTTTTCATGATTTACGTCCACACCAAAATGATG	639
DB	484	ATGAGTCTGCTCAAGCGGCTCGGCGATTTATGATCTACGTGTCATTCGAATTC	543
QY	640	TTGACGAT 647	
DB	544	TGATGAT 551	
RESULT 9			
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ID	AAH47118	standard;	DNA; 1997
XX	AAH47118;		
XX	18-OCT-2000	(first entry)	
XX	Arabidopsis	thaliana	DNA fragment SEQ ID No: 52628.
XX	Hybridisation	assay;	genetic mapping; gene expression control;
XX	protein	identification;	signal transduction pathway;
XX	metabolic	pathway;	promoter; termination sequence; ss.
XX	Arabidopsis	thaliana.	
XX	EF1033405-A2.		
XX	06-SEP-2000.		
XX	25-FEB-2000;	2000EP-0301439.	
XX	25-FEB-1999;	99US-0121425.	
XX	05-MAR-1999;	99US-0123180.	
XX	09-MAR-1999;	99US-0124548.	
XX	23-MAR-1999;	99US-0125788.	
XX	25-MAR-1999;	99US-0126264.	
XX	29-MAR-1999;	99US-0126785.	
XX	01-APR-1999;	99US-0127462.	
XX	06-APR-1999;	99US-0128234.	

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PR 12-OCT-1999: 990S-0159293.
PR 13-OCT-1999: 990S-0159294.
PR 13-OCT-1999: 990S-0159294.

CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful
CC for enhancing or inhibiting production of a biosynthetic product in a
CC plant. (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=999909770445.

XX Sequence 833 BP: 242 A; 187 C; 159 G; 245 T; 0 other;

Query Match 13.2%; Score 103.6; DB 24; Length 833;
Best Local Similarity 57.5%; Pred. No. 1.2e-22;
Matches 215; Conservative 0; Mismatches 144; Indels 15; Gaps 1;

QY 369 GGTCTCCGACASAGTGGATCACTGCAAGCTATATTAGACTGCGACAGAGGACCATGGAG 428

DB 832 GCGGACCCCAAGTCTGCGCCCTGCGAAGAAATCTATATTGCGACAGCAAACTATGCCAG 773

QY 429 ATGATGTACAGCATGTGATTGAGGCTCTCAGGGCTTCAGGGCTTCAGGGCCGGAAGATCCAGA 488

DB 772 ATGATGTATGATGTTTATAGCAAAAGAACTGGAAGCGGTGCAATCATGATGCTCATCTCTC 713

QY 489 AACTATCTGACATCTCTCTGCTTGTGAAACCGGTGAGGTCAAGAAAGATGCGAGATGAG 548

DB 712 GATTACCTTAACTTTTACTTGCTTGTGTAACGAGAGCAGCTTCCAGATGATGCCAGCC 653

QY 549 CGTGTGTGAGAAACGACAGCCGCGACACTGATTACATGAGGCGCGCAAGAACGCGGTTC 608

DB 652 ACCAATGGCAGTCGTGATCAGATCTTATATTTCCAG-----CGTTTC 608

QY 609 ATGATTAGTCTCACACCAAAATGATCACTGTTGAGGATGATATATATCATTTGGTCT 668

DB 607 ATGATTAGTCTGACGCAAAAGGGATGATGATGATGATGATGATGATGATGATGATGAT 548

QY 669 GCTAACATCAACCCAGAGGTCAATGGACGCTGGAAGAGACTCTCAGATAGCAATGGAGCT 728

DB 547 GCTAATATCAACCAAGATCTATGGCAGGCAACCAAGATAGTAAATGCCATGGCGCA 488

QY 729 TATCAACCATCA 742

DB 487 TACCAACCTAATCA 474

RESULT 14

ABL93878

ID ABL93878 standard; cDNA: 452 BP.

XX ABL93878;

DT 10-JUN-2002 (first entry)

XX Arabidopsis thaliana nucleic acid sequence Ref:2027643 SEQ ID NO:643.

XX Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;

KW Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;

KW genetic modification; gene; ss.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX US2002023280-A1.

PN 21-FEB-2002.

PD 26-JAN-2001; 2001US-0770444.

XX 27-JAN-2000; 2000US-174502P.

PR (GORLACH J. PA

XX (ANYA) AN Y. PA

PA (HAM) HAMILTON C. M. PA

PA (PRIC) PRICE J. L. PA

PA (RAIN) RAINES T. M. PA

PA (YUY) YU Y. PA

PA (RAME) RAMEAKA J. G. PA

PA (PAGE) PAGE A. PA

PA (MATH) MATHIEU A. V. PA

PA (LEDF) LEDFORD B. L. PA

PA (WOES) WOESSNER J. P. PA

PA (HAAS) HAAS W. D. PA

PA (GARC) GARCIA C. A. PA

PA (KRICK) KRICKER M. PA

PA (SLAT) SLATER T. PA

PA (DAVI) DAVIS K. R. PA

PA (ALLE) ALLEN K. PA

PA (HOFF) HOFFMAN M. PA

PA (HURH) HURBAN P. PA

XX Goriach J., An Y., Hamilton CM., Price JL., Raines TM., Yu Y.,

PI Rameaka JG., Page A., Mathew AV., Ledford BL., Woessner JP., Haas WD,

PI Garcia CA., Kricker M., Slater T., Davis KR., Allen K., Hoffman N,

PI Hurban P;

XX WPI: 2002-267486/31.

DR New Arabidopsis thaliana nucleic acid, for identifying homologous

XX genes, producing compositions that modulate the expression or function

PT of its encoded protein, and mapping functional regions of a protein -

PT Claim 1: SEQ ID 643; 44pp; English.

XX The present invention describes an Arabidopsis thaliana nucleic acid (1)

PS comprising a sequence capable of hybridising under stringent conditions

CC to a sequence (S1) selected from any one of the 999 sequences given in

CC ABL93236 to ABL94234. (1) have insecticide and fungicide activities, and

CC they can be used as protein expression modulators. (1) can be used in

CC identifying homologous or related genes, in producing compositions that

CC modulate the expression or function of their encoded proteins, mapping

CC functional regions of the proteins, and in studying associated

CC physiological pathways. (1) can also be used: (1) for the genetic

CC manipulation of cells, particularly plant cells; (2) in screening assays

CC of various plant strains to determine the strains that are best capable

CC of withstanding a particular disease or environmental stress; (3) for

CC enhancing or inhibiting production of a biosynthetic product in a plant;

CC (4) as probes in mapping and in diagnosis, in genetic modification and

CC for screening purposes, to generate additional copies of the nucleic

CC acids, to generate ribozymes or antisense oligonucleotides, and as

CC single-stranded DNA probes or as triple strand forming oligonucleotides;

CC and (5) for generating genetically modified transgenic organisms.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the

CC USPTO web site.

XX Sequence 452 BP: 136 A; 86 C; 106 G; 124 T; 0 other;

SQ Query Match 12.5%; Score 97.8; DB 24; Length 452;

Best Local Similarity 56.1%; Pred. No. 6.5e-21;

Matches 245; Conservative 0; Mismatches 162; Indels 30; Gaps 2;

QY 277 TAATCCCAAGAGTGTGCGTCGAACATAGTACGAACATGATCAAGCAAGACAGATCTCA 336

DB 16 TAATCCGATGGAATCGCGTGAAGATTCCTAAATAAAATTAAGCAAGCAAGAAATTTG 75

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QM nucleic - nucleic search, using sw model

Run on: May 4, 2003, 21:56:05 ; Search time 2336.79 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 41: em_htgo_other.*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	783	100.0	2794	8	ATU36381	U36381 Arabidopsis
2	738.6	94.3	1886	8	AF428278	AF428278 Arabidops
3	644.6	82.3	81370	8	AB017071	AB017071 Arabidops
4	593	75.7	2793	8	AF090445	AF090445 Brassica
5	588.2	75.1	2702	8	AF090444	AF090444 Brassica
6	588.2	75.1	2743	8	BOU85482	BOU85482 Brassica ol
7	489.6	62.5	2808	8	KCCPLD	L33686 Ricinus com
8	481.4	61.5	2911	8	VUU92656	U92656 Vigna unqui
9	478.4	61.1	2834	6	166478	166478 Sequence 1
10	469	59.9	3404	8	AF113918	AF113918 Brassica
11	461.6	59.0	3614	8	AF113919	AF113919 Brassica
12	454.8	58.1	1918	8	AF451979	AF451979 Papaver s
13	453.2	57.9	1875	8	AF451980	AF451980 Papaver s
14	445.8	56.9	2990	8	KICPHD2	173411 oryza sativ
15	445.8	56.9	3040	6	AK005011	AK005011 Sequence
16	445.8	56.9	3040	6	AK037062	AK037062 Sequence
17	445.8	56.9	3040	6	AK082616	AK082616 Sequence
18	441	56.3	2697	8	AY013252	AY013252 Lycopersi
19	439.4	56.1	2427	8	AF201661	AF201661 Lycopersi
20	438.2	56.0	2723	8	NT84822	284822 Nicotiana t
21	437.2	55.8	117737	8	F608	AC008016 Arabidops
22	434.6	55.5	2848	8	AF154425	AF154425 Lycopersi
23	425	54.3	2793	8	MZEPHD1	173410 Zed mays mk
24	425	54.3	2804	6	AK005012	AK005012 Sequence
25	424.4	54.2	2859	8	PB096438	P96438 Pimpinella
26	419.2	53.5	2829	8	AY013253	AY013253 Lycopersi
27	405.8	51.8	2674	8	CPI133001	AI14001 Craterost
28	404.2	51.6	2662	8	CPI133000	AI14000 Craterost
29	386.4	49.3	5676	8	RC072693	U72693 Ricinus com
30	363.4	46.4	93127	2	AC122167	AC122167 Medicago
31	360.8	46.1	2397	8	AF451981	AF451981 Papaver s
32	359.2	45.9	2067	8	AF451982	AF451982 Papaver s
33	358.2	45.7	2903	8	AY013254	AY013254 Lycopersi
34	347.2	44.3	5871	8	AB001920	AB001920 oryza sat
35	347.2	44.3	135295	8	AP003282	AP003282 oryza sat
36	342.8	39.9	148906	2	AP003629	AP003629 oryza sat
37	296.6	37.9	5169	8	AB001919	AB001919 oryza sat
38	269.8	34.5	4740	8	AF271357	AF271357 oryza sat
39	264	33.7	148054	2	AC087553	AC087553 oryza sat
40	260.6	33.3	110469	8	AC006258	AC006258 Arabidops
41	252.4	32.2	6672	8	AF271356	AF271356 oryza sat
42	252.4	32.2	148906	2	AP003629	AP003629 oryza sat
43	244.2	31.2	113663	2	AC094323	AC094323 oryza sat
44	237.2	30.3	551	6	AX150726	AX150726 Sequence
45	237.2	30.3	551	6	AX155014	AX155013 Sequence

ALIGNMENTS

RESULT 1
ATU36381
LOCUS
DEFINITION Arabidopsis thaliana phospholipase D mRNA, complete cds.
ACCESSION U36381
VERSION U36381.1
KEYWORDS
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 2794)
AUTHORS Dyer J.H., Zeng L. and Wang X.
TITLE Cloning and Nucleotide Sequence of a cDNA (Accession No. U36381)

[illegible]

Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tan, C.C., Tortum, M., Yamada, K., Yamamura, Y., Yu, S., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES		Location/Qualifiers	
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	Best local Similarity	98.1%	Pred. No. 1.4e-210;
	Matches	758; Conservative	0; Mismatches 14; Indels 1; Gaps 1;
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	Db	558	GACCACGATGTCGAATGTCACATCTTTAGTTCATGATGAGGAGCTGCTGCTGGG 617
	QY	71	TTTCCCGAGTCGCTGAAGCTGCTGGCGAAGCGGGCTTACAGTGGGAAGATACAT 130
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	QY	131	CATTGATAGAGTATCCAGATGCTTACATTCATGCAATCAGAGTCTAAGGATTTTCAT 190
	Db	677	CATTGATAGAGTATCCAGATGCTTACATTCATGCAATCAGAGTCTAAGGATTTTCAT 736
	QY	191	CIAGTTTCAAAACAGTACCTTCCTTGGAGTCTTTTTCCTTGGCAGCCCATGATTAC 250
	Db	737	CIAGTTTCAAAACAGTACCTTCCTTGGAGTCTTTTTCCTTGGCAGCCCATGATTAC 796
	QY	251	TCTTCAGACATCAATGCCCTGCCACTTAATCCCAAAAGAGTGTGCTGAAGATAGTAG 310
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	QY	311	CAAGATTGATCAAGGAGAGATTCAGGGTCTATGTTGTGTTTCCCAATGTGGCAGAGG 370
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	QY	371	TCTCCAGAGTGCATCAGTCCAGGTATATTAGATGCGCAGAGGAGCCATGGAGAT 430
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	QY	431	GATTCAGAGGATGTGATTCAGGCTCTCAAGGCTCTTTCAGGCGCCGCAAGATCCAGAAA 490
	Db	977	GATTCAGAGGATGTGATTCAGGCTCTCAAGGCTCTTTCAGGCGCCGCAAGATCCAGAAA 1036
	QY	491	CTATCTGACATCTCTCTGCTTGGAAACCGTGAGGTCAGAGAACAGATGAGTAGTAGGCC 550

Db	1037	CTATCTGACATCTCTCTGCTTGGAAACCGTGAGGTCAGAGAACAGATGAGATGAGGCC 1096	
QY	551	TGCTGAGAAACAGACCCGACACTCATTACATGAGGCGTGCAGAAAGCATGCTGCTTTCAI 610	
Db	1097	TGCTGAGAAACAGACCCGACACTCATTACATGAGGCGTGCAGAAAGCATGCTGCTTTCAI 1156	
QY	611	GATTACGTCACACCAAAATGATGATGCTGACATGAAATATATTATCATGAGGCTGCTGC 670	
Db	1157	GATTACGTCACACCAAAATGATGATGCTGACATGAAATATATTATCATGAGGCTGCTGC 1216	
QY	671	TACATCAGACGAGGTCATGAGGTCGAGAGATCTCTGAGATATATATGAGAGATTA 740	
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QY	731	TCAACACATCAGCTTCTCCATAGACACACGCTGCTGAGGTCATGATGAGGT 784	
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DEFINITION	Arabidopsis thaliana genomic DNA, chromosome 3, pl clone: MSJ11.		
ACCESSION	AB017071 RA000014		
VERSION	AB017071.1 GI:3510347		
KEYWORDS	Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui pl clone:MSJ11.		
SOURCE	Arabidopsis thaliana		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; brassicaceae; Arabidopsis. 1 (sites)		
AUTHORS	Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E. and Tabata, S.		
TITLE	Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty pl and TAG clones		
JOURNAL	DNA Res. 7 (2), 141-145 (2000)		
MEDLINE	20277480		
REFERENCE	2 (bases 1 to 81470)		
AUTHORS	Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E. and Tabata, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1542-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:yakamura-kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-4944)		
COMMENT	Address for correspondence: kaoskazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/and-graph.cgi?c=MSJ11 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/grail-1.3/), GENSCAN (Chris Burge, MIT, http://cck-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hedgeshaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://aremlinf.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is M0D17 and the 3' clone is M0C18.		
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complement (join(2827, 3005, 3184, 3279, 3361, 3448,
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Best Local Similarity 88.4%; Pred. No. 3.6e-182;
Matches 758; Conservative 0; Mismatches 14; Indels 85; Gaps 2;

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Db 41681 GACCACGATGTCGTAATGCCAATTCCTTAGGTCCTTATGAGTCCATTCATGACGAGCGTCTGCTGGG 41740
QY 71 TTTCCCGAGTCGCTGAAGTCGTCGCGAAGCCCGGCTTGTACAGTGGGAAAGATAACAT 130
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QY 191 CTAGCTTCAAAACAGTACTTCCTTTGGAGTCTTTTCTTGGCAGCCGATGGTATTAC 250
Db 41860 CTAGCTTCAAAACAGTACTTCCTTTGGAGTCTTTTCTTGGCAGCCGATGGTATTAC 41919
QY 251 TCTCAGACATCAATGCCCTGCCACTTAATCCCAAGAGTGTGCTGAAGATAGTAG 310
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QY 311 CAAGATTGATCAAGGAGAGATTCAGGGCTCTATGTTGTTGTTTCAATGTGGCAGAGG 370
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RESULT 4

AF090445 2793 bp mRNA linear PLN 20-NOV-1998
LOCUS AF090445
DEFINITION Brassica oleracea phospholipase D1 (PLD1) mRNA, complete cds.

ACCESSION AF090445
VERSION AF090445.1 GI:3639088
KEYWORDS
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 2793)
AUTHORS Pannenberg, J., Mansfeld, J. and Ulbrich-Hofmann, K.
TITLE Identification of Two Isoenzymes (Accession Nos. AF090444 and AF090445) of Phospholipase D from cabbage (brk48-188)
JOURNAL Plant Physiol. 118 (3), 1102 (1998)
REFERENCE 2 (bases 1 to 2793)
AUTHORS Pannenberg, J., Mansfeld, J. and Ulbrich-Hofmann, K.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1998) Biochemistry/Biotechnology, M. Luther
UNIVERSITY, Kurt Mothes-Strasse 3, Halle 06120, Germany
FEATURES
Location/Qualifiers
1..2793

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/cultivar="capitata (Lamex)"
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BASE COUNT 720 a 659 c 700 q 714 t

Query Match 75.7%; Score 593; DB 8; Length 2793;
Best Local Similarity 86.3%; Pred. No. 8.2e-167;
Matches 667; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY 11 GACCACGATGTCGTAATGCCAATTCCTTAGGTCCTTATGAGTCCATTCATGACGAGCGTCTGCTGGG 70
Db 1455 GATCAGCAGCGTGTGAATGTGCACTGCTTTAGATCATCATGAGTGCAGTCTGCTGTGG 1514
QY 71 TTTCCCGAGTCGCTGAAGTCGTCGCGAAGCCCGGCTTGTACAGTGGGAAAGATAACAT 130
Db 1515 TTTCCCGAGTCGCTGAAGTCGTCGCGAAGCCCGGCTTGTGCTTGGGAAAGATAACAT 1573
QY 131 CATTCATAGGATATCAAGATGCTTACATTCATGCAATCAGAGTCTTAAAGATTTCAT 140
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Db 1634 CTAGCTTCAAAACAGTACTTCCTTTGGAGTCTTTTCTTGGCAGCCGATGGTATTAC 1693
QY 251 TCTCAGACATCAATGCCCTGCCACTTAATCCCAAGAGTGTGCTGAAGATAGTAG 310
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[illegible]

RESULTS

AF090444	LOCUS	2702 bp	mRNA	linear	PLN 20-NOV-1998
	DEFINITION	brassicaceae oleacea phospholipase D2 (PLD2) mRNA, complete cds.			
	ACCESSION	AF090444			
	VERSION	AF090444.1	GI: 3649086		

SOURCE	ORGANISM
	<i>Brassica oleracea</i> .
	<i>Brassica oleracea</i> .
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
	Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

AUTHORS Panenderg, I., Maunfeld, J., and Ulbricht-Hoimann, R.
TITLE Identification of Two Isozymes (Accession NOS. AF090444 and AF090445) of Phospholipase D from Cabbage (UCR98-188)
JOURNAL Plant Physiol. 118 (4), 1102 (1998)
REFERENCE 2 (bases 1 to 2702)

AUTHORS Rannenberg, I., Mansfeld, J., and Ulfdrich Hoffmann, R.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1998) Biochemistry/Biotechnology, M.-Luther
FEATURES University, Kurt-Meibohm-Strasse 4, Halle 06120, Germany
Location/Qualifiers

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1. 2702
/ordinism "Brassica oleracea"
/cultivar = "capitata (lemon)"
/db_xref: "taxon: 4712"
1. 2702

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/zone = pl12"
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[illegible]

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 VERSION U85482.1 GI:3924620
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 ORGANISM Brassica oleracea var. capitata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 2743)
 Kim,D.U., Roh,T.Y., Lee,J., Noh,J.Y., Jang,Y.J., Hoe,K.L., Yoo,H.S.
 and Choi,M.U.
 Molecular cloning and functional expression of a phospholipase D
 from cabbage (Brassica oleracea var. capitata)
 Biochim. Biophys. Acta 1437 (3), 409-414 (1999)
 99203163
 10101274
 2 (bases 1 to 2743)
 Kim,D.U., Lee,J.E., Roh,T.Y., Choi,M.-U. and Yoo,H.S.
 Direct Submission
 Submitted (15-JAN-1997) Chemistry, Seoul National University,
 Shinkim-dong, Kwan-Ak-Gu, Seoul, Korea
 3 (bases 1 to 2743)
 Kim,D.U., Lee,J.E., Roh,T.Y., Choi,M.-U. and Yoo,H.S.
 Direct Submission
 Submitted (24-NOV-1998) Chemistry, Seoul National University,
 Shinkim-dong, Kwan-Ak-Gu, Seoul, Korea
 Sequence update by submitter
 On Nov 24, 1998 this sequence version replaced gi:2737998.
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 ACCESSION L33686
 VERSION L33686.1 GI:1438074
 KEYWORDS phospholipase D.
 ORGANISM Ricinus communis (strain hale) cDNA to mRNA.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Malpighiales; Euphorbiales; Ricinus.
 1 (bases 1 to 2808)
 Wang,X., Xu,L. and Zheng,L.
 Cloning and expression of phosphatidylethanolamine-hydrolyzing
 phospholipase D from Ricinus communis L.
 J. Biol. Chem. 269 (32), 20412-20417 (1994)
 94327597
 8051126
 2 (bases 1 to 2808)
 Wang,X.
 Direct Submission
 Submitted (24-AUG-1994) Xermin Wang, Department of Biochemistry,
 Kansas State University, Manhattan, KS 66506, USA
 3 (bases 1 to 2808)
 Wang,X.
 Direct Submission
 Submitted (18-JUL-1996) Xuemin Wang, Department of Biochemistry,
 Kansas State University, Manhattan, KS 66506, USA

BASE COUNT	840 a	556 c	674 g	841 t	
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ACCESSION	I66478				
VERSION	I66478.1				G1:2724455
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SOURCE					
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2834)				
AUTHORS	Wang, X				
TITLE	Recombinant DNA sequences encoding phospholipase				
JOURNAL	Patent: US 5670366-A 1 23-SEP-1997				
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Db 1986 TTTCTGATCAGCTGAAGTAGCTGTGGAAGCTGTGGAAGCTGTGGAAGCTGTGGAAG 2044

QY 131 CATTGATAGGAGTATCCAAAGATGCTTACATTCATGCAATCAGACGCTGCTAAGGATTCAT 190

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QY 311 CAAGATTGATCAAGCAGAGAGTTCAGGCTCTATGTTGTTTCCAAATGTCGCAAGG 370

Db 2225 CAAGATGAGAAAGCAGAGAGTTTAGGTTTATGTTGTTTCCAAATGTCGCAAGG 2284

QY 371 TCTCCAGAGAGTGCATGTCGCAAGCTATATAGACTGCGCAGAGGAGCAGATGAGAT 430

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QY 431 GATGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490

Db 2445 GATGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2404

QY 491 CTATCTGACATCTCTCTGCTTGGAAACCGTGGGTCAGAAAGAGATGAGAGTATGAGCC 550

Db 2405 CTATCTGACATCTCTCTGCTTGGAAACCGTGGGTCAGAAAGAGATGAGAGTATGAGCC 2464

QY 551 TCGTGAGAAACAGACCCGACACTGATACATGAGGGGTCAGAAAGAGATGAGAGTATGAGCC 610

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ACCESSION AF451979
VERSION AF451979.1 GI:17933368
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SOURCE Papaver somniferum.
ORIGIN Papaver somniferum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Papaveraceae; Papaver.
1 (bases 1 to 1918)
Lerchner, A., Schaeffner, I., Weissova, K. and Ulbrich-Hofmann, K.
Identification of two isoenzymes of phospholipase D from opium poppy
unpublished
2 (bases 1 to 1918)
Lerchner, A., Schaeffner, I., Weissova, K. and Ulbrich-Hofmann, K.
Direct Submission
Submitted (23-Nov-2001) M.-Luther University, Kurt-Mothes Str. 3, Halle 06120, Germany
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FEATURES
Source

gene

CDS

BASE COUNT 539 a 377 c 441 g 561 t

ORIGIN

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Best local Similarity 75.1%; Pred. No. 2.8e-125;

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QY 70 GTTTCGGAGTCCGCTGCAAGCTGTCGGAAGCGGGCTGTGACATGCGGAAGATAACA 129

Db 679 ATTCCCTGATTCACCTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 747

QY 130 TCATCATAGAGATATCCAGATGCTTATATTCATGCAATGATGATGATGATGATGAT 189

Db 738 TCATCATAGAGATATCCAGATGCTTATATTCATGCAATGATGATGATGATGATGAT 747

QY 190 TCTACGTGGAAGATGAGTATTCCTGAGAGTCTTTCCTGAGAGTCTTTCCTGAGAGT 249

Db 798 TTTACATAGAAATCATGATTTCTGCGAAGTTCATAGCTGAGAGATGAGATGAGAT 857

QY 250 CTGCTGAGGACATCAATGCTGCTGCTTAAATGCAAAAGAGTGTGCTGCAATGATTA 309

Db 858 AGCTGAGGAAATAAAGCTGCTGCTTATTCGAAAGAAATCTCATTAAATATCTTA 917

QY 310 GCAAGATTTGATTAAGAGAGATGAGTTCAGAGTCTGATTTCTGAGTCTGAGTCTGAG 969

Db 918 GCAAGATTTGATTAAGAGAGATGAGTTCAGAGTCTGATTTCTGAGTCTGAGTCTGAG 977

QY 370 GTCTCCAGAGAGTGTGATCAGTCTCAAGCTATATTAATGAGAGAGAGAGATGAGAT 429

Db 978 GTATCCAGAGAGTGTGATCAGTCTCAAGCTATATTAATGAGAGAGAGAGATGAGAT 1037

QY 430 TGATGTACAAGGATGTGATTCAGGCTCTCAAGGCTCTTGAAGGCTCTGAGGCTCTGAG 489

REFERENCE 1 (bases 1 to 2990)
AUTHORS Ueki,J., Morioka,S., Komari,T. and Kumashiro,T.
TITLE Purification and characterization of phospholipase D (PLD) from rice (Oryza sativa L.) and cloning of cDNA for PLD from rice and maize (Zea mays L.)
JOURNAL Plant Cell Physiol. 36 (5), 903-914 (1995)
MEDLINE 96012933
REFERENCE 2 (bases 1 to 2990)
AUTHORS Ueki,J.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1995) Jun Ueki, Japan Tobacco Inc., Plant Breeding and Genetics Research Lab; 700 Higashibara, Iwata, Shizuoka 438-0802, Japan (E-mail:Jun.Ueki@pbjrl.jti.co.jp, Tel:81-538-32-7111, Fax:81-538-32-8700)
FEATURES
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CLNRMVQKAGEYQPEQADTDYRAGEARFMYVHTKMMIVDVEYIIIGSANIN
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LGAKSDYMPILIS"
BASE COUNT 734 a 724 c 783 g 749 t
ORIGIN

Query Match 56.9%; Score 445.8; DB 8; Length 2990;
Best Local Similarity 74.0%; Pred. No. 1.5e-122;
Matches 578; Conservative 0; Mismatches 202; Indels 1; Gaps 1;

Qy 3 TTCCAGAGACACAGATGTGTGGAAATGTCACATTTTAGTGTCCATTTGAGGAGAGCTG 62
Db 1551 TTCCAGAGGACAGAGAAACATGAATGTTACGCTATTATAGATCATTGATGGTGTCTG 1610

Qy 63 CTGCTGGGTTTCCCGAGTGCCTGAAGCTGCTGGGAGCGGGCTGTACAGATGGGAAA 122
Db 1611 CTTTGGGTTCCCTGATACCCCTGAGGAGGCTGCAAAAGCTGGCTTGTA-AGCGGAAAG 1669

Qy 123 GATAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 182
Db 1670 GATCAAAATCATGACAGAGGATCATGAGATGATGATGATGATGATGATGATGATG 1729

Qy 183 GATTTCATCTACGTTGAAACACGATCTCTCTGGGAGTTCTTTTGGTGGGACCGGAT 242
Db 1730 AACTTCATCTATATAGACAACCAATCTCTCTGGGAGTTCTCTATGCTTGAACCCGAG 1789

Qy 243 GATTTCATCTACGTTGAAACACGATCTCTCTGGGAGTTCTTTTGGTGGGACCGGAT 302
Db 1790 GGCATCAAGCTGAGACATTTGGTCCCTGCTGATTTGATTTCTTAAGGAGCTTGCAC 1849

Qy 303 ATAGTTAGCAAGATTGATCAAGAGAGAGAGTTCAGGCTGATGTTGGTTCCTCAATGG 362
Db 1850 GTTGCACTAGATTGAAGCCGGGAGGCTTCACTGTTTATGTTGGTGGCCCAATGG 1909

Qy 463 GCAGAAAGTCTCCAGAGAGTGGATCAGTGCAGGCTATATATAGACTGGCAGGAGGACC 422

Db 1910 CCTGAGGGTGTTCACAGAGATGGATCTGTTCAGGCAATCTGACACTGGCAAAAGAGAAC 1969

Qy 423 ATGAGATCATGTATACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 482

Db 1970 ATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2029

Qy 483 CCAAGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 542

Db 2030 CCAAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2089

Qy 543 ATGAGAGCTGCTGAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 602

Db 2090 TATCAGCTGAGAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2149

Qy 603 CGTTTCATGATTTACGTCACACCAAAATGATGATGATGATGATGATGATGATGATGAT 662

Db 2150 AGTTTCATGATTTATGTCACACCAAAATGATGATGATGATGATGATGATGATGATGAT 2209

Qy 663 GGGTCTCTAACATCAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 722

Db 2210 GGTTCTGCAACATCAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2269

Qy 723 GGAGGTTATCAACACATCACTTTGTCACATGAGAGAGAGAGAGAGAGAGAGAGAGAG 782

Db 2270 GGGGGTACAGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2429

Qy 783 T 783

Db 2330 T 2330

RESULT 15

AR005011 AR005011 Sequence 1 from patent US 5747327. Linear PAT 04-DEC-1998

LOCUS AR005011

DEFINITION AR005011

ACCESSION AR005011

VERSION AR005011.1 GI:3965890

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3040)
AUTHORS Ueki,J. and Morioka,S.
TITLE Phospholipase D gene originated from plant
JOURNAL Patent: US 5747327-A 1 05-MAY-1998;
FEATURES Location/Qualifiers
source 1..3040
/organism="unknown"
BASE COUNT 784 a 724 c 783 g 749 t
ORIGIN

Query Match 56.9%; Score 445.8; DB 6; Length 3040;
Best Local Similarity 74.0%; Pred. No. 1.5e-122;
Matches 578; Conservative 0; Mismatches 202; Indels 1; Gaps 1;

Qy 3 TTCCAGAGACACAGATGTGTGGAAATGTCACATTTTAGTGTCCATTTGAGGAGAGCTG 62
Db 1551 TTCCAGAGGACAGAGAAACATGAATGTTACGCTATTATAGATCATTGATGGTGTCTG 1610

Qy 63 CTGCTGGGTTTCCCGAGTGCCTGAAGCTGCTGGGAGCGGGCTGTACAGATGGGAAA 122
Db 1611 CTTTGGGTTCCCTGATACCCCTGAGGAGGCTGCAAAAGCTGGCTTGTA-AGCGGAAAG 1669

Qy 123 GATAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 182
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Qy 183 GATTTCATCTACGTTGAAACACGATCTCTCTGGGAGTTCTTTTGGTGGGACCGGAT 242
Db 1730 AACTTCATCTATATAGACAACCAATCTCTCTGGGAGTTCTCTATGCTTGAACCCGAG 1789

Qy 243 GATTTCATCTACGTTGAAACACGATCTCTCTGGGAGTTCTTTTGGTGGGACCGGAT 302
Db 1790 GGCATCAAGCTGAGACATTTGGTCCCTGCTGATTTGATTTCTTAAGGAGCTTGCAC 1849

Qy 303 ATAGTTAGCAAGATTGATCAAGAGAGAGAGTTCAGGCTGATGTTGGTTCCTCAATGG 362
Db 1850 GTTGCACTAGATTGAAGCCGGGAGGCTTCACTGTTTATGTTGGTGGCCCAATGG 1909

Qy 463 GCAGAAAGTCTCCAGAGAGTGGATCAGTGCAGGCTATATATAGACTGGCAGGAGGACC 402

